```
=> fil capl; d que l1
FILE 'CAPLUS' ENTERED AT 12:23:49 ON 23 FEB 2005
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FILE COVERS 1907 - 23 Feb 2005  VOL 142 ISS 9
FILE LAST UPDATED: 22 Feb 2005  (20050222/ED)
```

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

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L1          7 SEA FILE=CAPLUS ABB=ON  KERMANI B?/AU
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inventor search

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=> fil wpids; d que l48
FILE 'WPIDS' ENTERED AT 12:23:50 ON 23 FEB 2005
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FILE LAST UPDATED:            18 FEB 2005      <20050218/UP>
MOST RECENT DERWENT UPDATE:      200512        <200512/DW>
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    FOR DETAILS. <<<


L34            26 SEA FILE=WPIDS ABB=ON  KERMANI B?/AU
L35          3564 SEA FILE=WPIDS ABB=ON  ALLELE#
L36          2764 SEA FILE=WPIDS ABB=ON  GENOTYP?
L37        156518 SEA FILE=WPIDS ABB=ON  ARRAY#
L38          3468 SEA FILE=WPIDS ABB=ON  MICROARRAY#
L39         15854 SEA FILE=WPIDS ABB=ON  NORMALI?
L40          7980 SEA FILE=WPIDS ABB=ON  (COORDINATE OR CO ORDINATE)(2A)SYSTEM#
L41            15 SEA FILE=WPIDS ABB=ON  SWEEP POINT#
L42          3946 SEA FILE=WPIDS ABB=ON  CONTROL POINT#
L43           581 SEA FILE=WPIDS ABB=ON  (REGISTRATION OR CONFORMATION? OR
                  PROJECT?)(3A)TRANSFORM?
L44            31 SEA FILE=WPIDS ABB=ON  DELAUNAY
L45          1584 SEA FILE=WPIDS ABB=ON  TRIANGULAT?
L46            49 SEA FILE=WPIDS ABB=ON  GENETIC DATA#
L47             4 SEA FILE=WPIDS ABB=ON  L34 AND (L35 OR L36 OR L37 OR L38 OR
                  L39 OR L40 OR L41 OR L42 OR L43 OR L44 OR L45 OR L46)
L48             3 SEA FILE=WPIDS ABB=ON  L47 NOT CLOCK#


=> fil JICST-EPLUS, PASCAL, BIOTECHNO, ESBIOBASE, BIOSIS, DISSABS, JAPIO,  INSPEC,
COMPENDEX, COMPUSCIENCE, COMPUAB, SCISEARCH
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FILE 'JICST-EPLUS' ENTERED AT 12:23:51 ON 23 FEB 2005

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FILE 'BIOSIS' ENTERED AT 12:23:51 ON 23 FEB 2005

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FILE 'JAPIO' ENTERED AT 12:23:51 ON 23 FEB 2005

FILE 'INSPEC' ENTERED AT 12:23:51 ON 23 FEB 2005

FILE 'COMPENDEX' ENTERED AT 12:23:51 ON 23 FEB 2005

FILE 'COMPUSCIENCE' ENTERED AT 12:23:51 ON 23 FEB 2005

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=> d que 174

L61          42 SEA KERMANI B?/AU
L62      315958 SEA ALLELE#
L63      367676 SEA GENOTYP?
L64     1845597 SEA GENETIC
L65      691272 SEA ARRAY#
L66       55463 SEA MICROARRAY#
L67      302708 SEA NORMALIZ? OR NORMALIS?
L68       41265 SEA (COORDINATE OR CO ORDINATE)(W) SYSTEM#
L69          19 SEA SWEEP POINT#
L70       16525 SEA CONTROL POINT#
L71        5953 SEA DELAUNAY
L72       30643 SEA TRIANGULAT?
L73        6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?)(3A) TRANSFORM?
L74          23 SEA L61 AND (L62 OR L63 OR L64 OR L65 OR L66 OR L67 OR L68 OR
                L69 OR L70 OR L71 OR L72 OR L73)

=> dup rem l1,174,148

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PROCESSING COMPLETED FOR L1
PROCESSING COMPLETED FOR L74
PROCESSING COMPLETED FOR L48
L91            18 DUP REM L1 L74 L48 (15 DUPLICATES REMOVED)
                  ANSWERS '1-7' FROM FILE CAPLUS
                  ANSWERS '8-10' FROM FILE PASCAL
                  ANSWERS '11-12' FROM FILE BIOSIS
                  ANSWER '13' FROM FILE DISSABS
                  ANSWER '14' FROM FILE INSPEC
                  ANSWER '15' FROM FILE COMPENDEX
                  ANSWER '16' FROM FILE COMPUAB
                  ANSWER '17' FROM FILE SCISEARCH
                  ANSWER '18' FROM FILE WPIDS

=> d ibib ed abs 1-7; d iall 8-18
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L91 ANSWER 1 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1

ACCESSION NUMBER: 2004:398783 CAPLUS
DOCUMENT NUMBER: 141:100629
TITLE: Decoding randomly ordered DNA arrays
AUTHOR(S): Gunderson, Kevin L.; Kruglyak, Semyon; Graige, Michael S.; Garcia, Francisco; **Kermani, Bahram G.**; Zhao, Chanfeng; Che, Diping; Dickinson, Todd; Wickham, Eliza; Bierle, Jim; Doucet, Dennis; Milewski, Monika; Yang, Robert; Siegmund, Chris; Haas, Juergen; Zhou, Lixin; Oliphant, Arnold; Fan, Jian-Bing; Barnard, Steven; Chee, Mark S.
CORPORATE SOURCE: Illumina, Inc., San Diego, CA, 92121, USA
SOURCE: Genome Research (2004), 14(5), 870-877
CODEN: GEREFS; ISSN: 1088-9051
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 17 May 2004
AB The authors have developed a simple and efficient algorithm to identify each member of a large collection of DNA-linked objects through the use of hybridization, and have applied it to the manufacture of randomly assembled arrays of beads in wells. Once the algorithm has been used to determine the identity of each bead, the microarray can be used in a wide variety of applications, including single nucleotide polymorphism genotyping and gene expression profiling. The algorithm requires only a few labels and several sequential hybridizations to identify thousands of different DNA sequences with great accuracy. The authors have decoded tens of thousands of arrays, each with 1520 sequences represented at .apprx.30-fold redundancy by up to .apprx.50,000 beads, with a median error rate of <1 + 10-4 per bead. The approach makes use of error checking codes and provides, for the first time, a direct functional quality control of every element of each array that is manufactured The algorithm can be applied to any spatially fixed collection of objects or mols. that are associated with specific DNA sequences.
REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 2 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2

ACCESSION NUMBER: 2003:654192 CAPLUS
TITLE: Automated information processing in randomly ordered arrays
INVENTOR(S): **Kermani, Bahram Ghaffarzadeh**; Haas, Juergen
PATENT ASSIGNEE(S): Illumina, Inc., USA

SOURCE: PCT Int. Appl.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003069333	A1	20030821	WO 2003-US4570	20030214

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-357213P P 20020214

ED Entered STN: 22 Aug 2003

AB The invention relates to the use of a computer system to compare images generated from a randomly ordered array. This system preserves the relative position of each site within the array so that the same site can be compared in different images.

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 3 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 2004:665013 CAPLUS
DOCUMENT NUMBER: 141:406396
TITLE: Highly parallel SNP genotyping
AUTHOR(S): Fan, J.-B.; Oliphant, A.; Shen, R.; **Kermani, B. G.**; Garcla, F.; Gunderson, K. L.; Hansen, M.; Steemers, F.; Butler, S. L.; Deloukas, P.; Galver, L.; Hunt, S.; McBride, C.; Bibikova, M.; Rubano, T.; Chen, J.; Wickham, E.; Doucet, D.; Chang, W.; Campbell, D.; Zhang, B.; Kruglyak, S.; Bentley, D.; Haas, J.; Rigault, P.; Zhou, L.; Stuelpnagel, J.; Chee, M. S.
CORPORATE SOURCE: Llumina, Inc., San Diego, CA, 92121, USA
SOURCE: Cold Spring Harbor Symposia on Quantitative Biology (2003), 68, 69-78
CODEN: CSHSAZ; ISSN: 0091-7451
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

ED Entered STN: 16 Aug 2004

AB A flexible, accurate, and scalable genotyping system, and have achieved high accuracy together with high call rates was developed. Conventional wisdom was that single-plex assays would be more accurate than highly multiplexed assay, and that it would be difficult to optimize assays in a multiplex format. In fact, the accuracy and call rates are similar to those obtained from single-plex genotyping systems, but at over 1,000 times the assay sequence complexity. These results demonstrate the specificity of the GoldenGate assay format, as well as the reproducibility and accuracy of the BeadArray platform and the BeadLab genotyping system as a whole. The Goldengate assay format is an exemplar for a new class of highly multiplexed assays that utilize parallel read about systems. It represents a significant departure from single and low-multiplex assays and is well suited for large-scale anal. of complex biol. systems.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 4 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2002:123361 CAPLUS
DOCUMENT NUMBER: 136:147506
TITLE: Automated information processing in randomly ordered arrays
INVENTOR(S): Stuelpnagel, John A.; Chee, Mark; Dickinson, Todd A.; Gunderson, Kevin; **Kermani, Bahram G.**
PATENT ASSIGNEE(S): Illumina, Inc., USA
SOURCE: PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2002012897	A2	20020214	WO 2001-US24882		20010809
WO 2002012897	C2	20030403			

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
CA 2419058	AA	20020214	CA 2001-2419058		20010809
AU 2001084760	A5	20020218	AU 2001-84760		20010809
PRIORITY APPLN. INFO.:			US 2000-636387	A	20000809
			WO 2001-US24882	W	20010809

ED Entered STN: 15 Feb 2002
AB The invention relates to the use of a computer system to compare images generated from a randomly ordered array. This system preserves the relative position of each site within the array so that the same site can be compared in different images.

L91 ANSWER 5 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:794199 CAPLUS
DOCUMENT NUMBER: 137:259628
TITLE: Automated information processing in randomly ordered arrays
INVENTOR(S): Stuelpnagel, John R.; Chee, Mark S.; Dickinson, Todd A.; **Kermani, Bahram G.**; Haas, Juergen
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 28 pp., Cont.-in-part of U.S. Ser. No. 636,387.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2002150909	A1	20021017	US 2001-925941		20010809
PRIORITY APPLN. INFO.:			US 1999-119323P	P	19990209
			US 2000-500555	A2	20000209

US 2000-636387 A2 20000809

ED Entered STN: 18 Oct 2002

AB The invention relates to the use of a computer system to compare images generated from a randomly ordered array. This system preserves the relative position of each site within the array so that the same site can be compared in different images.

L91 ANSWER 6 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:521036 CAPLUS
TITLE: Multi-dimensional optical disk
INVENTOR(S): **Kermani, Bahram Ghaffarzadeh**
PATENT ASSIGNEE(S): Lucent Technologies Inc., USA
SOURCE: Eur. Pat. Appl.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
EP 1117093	A2	20010718	EP 2000-311059		20001212
EP 1117093	A3	20021127			
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO					
US 6826143	B1	20041130	US 2000-482960		20000114
PRIORITY APPLN. INFO.:			US 2000-482960	A	20000114

ED Entered STN: 19 Jul 2001

AB The present invention provides an optical disk with pits and/or bumps which each contain a plurality of facets. Each facet of each pit and/or bump is intended for sep. read back as an individual 'side' of the optical disk (much as vinyl records had two 'sides' for sep. playback). The sep. 'sides' of the optical disk formed by sep. facets of each pit and/or bump can be read back either simultaneously or serially, either by a corresponding plurality of laser beams, or by a common laser beam which is positioned to a first orientation with respect to a rotating track to focus on a first set of facets of each pit and/or bump, and then repositioned to focus on a second set of facets of the same set of pits and/or bumps and thus to read a second 'side' of the optical disk. The technique may be extended to provide a single optical disk and even a single track of the optical disk with even more than two 'sides' by using three-, four- or five-sided pyramidal-shaped pits and/or bumps.

L91 ANSWER 7 OF 18 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:830504 CAPLUS
TITLE: Integrated circuit having reduced probability of wire-bond failure
INVENTOR(S): **Kermani, Bahram Ghaffarzadeh**
PATENT ASSIGNEE(S): Lucent Technologies Inc., USA
SOURCE: U.S., 9 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6153506	A	20001128	US 1999-263075	19990308
PRIORITY APPLN. INFO.:			US 1999-263075	19990308

ED Entered STN: 28 Nov 2000

AB The present invention provides an improved integrated circuit technique

for increasing the reliability of wire-bonds in an integrated circuit by increasing the contact angle between certain pins and their respective wire-bonds, particularly those pins otherwise most susceptible to wire-bond failure, i.e., those pins conventionally located toward the corners of a conventional integrated circuit. By doing so, the overall length of the wire-bonds in a chip will be reduced, which in turn can result in further reduction of the probability of wire-bond failures. In a disclosed embodiment, a five or more sided integrated circuit shape is introduced wherein pads on up to four sides of an integrated circuit wafer chip are bonded to pins supported on eight edges of an integrated circuit package. An integrated circuit having at least five pin-supporting edges renders more robust wire-bond angles for any given integrated circuit package size.

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L91 ANSWER 8 OF 18 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN DUPLICATE 6

ACCESSION NUMBER: 1999-0203912 PASCAL

COPYRIGHT NOTICE:

TITLE (IN ENGLISH): Using neural networks and **genetic** algorithms to enhance performance in an electronic nose

AUTHOR: **KERMANI B. G.**; SCHIFFMAN S. S.; NAGLE H. T.

CORPORATE SOURCE: Lucent Technologies, Allentown, PA 18103, United States; Department of Psychiatry, Duke University Medical Center, Durham, NC 27710-2159, United States; Department of Electrical and Computer Engineering, North Carolina State University, Raleigh, NC 27695-7911, United States

SOURCE: IEEE transactions on biomedical engineering, (1999), 46(4), 429-439, 49 refs.
ISSN: 0018-9294 CODEN: IEBEAX

DOCUMENT TYPE: Journal

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United States

LANGUAGE: English

AVAILABILITY: INIST-222E5, 354000074863020080

ABSTRACT: Sensitivity, repeatability, and discernment are three major issues in any classification problem. In this study, an electronic nose with an **array** of 32 sensors was used to classify a range of odorous substances. The collective time response of the sensor **array** was first partitioned into four time segments, using four smooth time-windowing functions. The dimension of the data associated with each time segment was then reduced by applying the Karhunen-Loeve (truncated) expansion (KLE). An ensemble of the reduced data patterns was then used to train a neural network (NN) using the Levenberg-Marquardt (LM) learning method. A **genetic** algorithm (GA)-based evolutionary computation method was used to devise the appropriate NN training parameters, as well as the effective database partitions/features. Finally, it was shown that a GA-supervised NN system (GANN) outperforms the NN-only classifier, for the classes of the odorants investigated in this study (fragrances, hog farm air, and soft beverages).

CLASSIFICATION CODE: 001D02C07; Applied sciences; Artificial intelligence
CONTROLLED TERM: Neural network; Improvement; Performance evaluation; **Genetic** algorithm; Sensitivity analysis; Reproducibility; Electronic nose; Artificial intelligence; System response; Olfactometry
BROADER TERM: Biomedical data processing

L91 ANSWER 9 OF 18 PASCAL on STN DUPLICATE 7
ACCESSION NUMBER: 2000-0146035 PASCAL
TITLE (IN ENGLISH): Novel method for reducing the dimensionality in a sensor **array**
AUTHOR: **KERMANI B. G.**; SCHIFFMAN S. S.; NAGLE H. T.
CORPORATE SOURCE: North Carolina State Univ, Raleigh NC, United States
SOURCE: IEEE Transactions on Instrumentation and Measurement, (1998), 47(3), 728-741, 18 refs.
ISSN: 0018-9456 CODEN: IEIMAO
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-222 G1
ABSTRACT: Specific types of gas sensors are normally produced by adding different dopants to a common substrate. The advancement of technology has made the fabrication of many dopants and consequently various sensors possible. As a result, in each family of gas sensors, one can find tens of different sensors which are only slightly different in the spectrum of response to various volatile compounds. The wide variety of available gas sensors creates a selection problem for any specific application. Sensor selection/reduction becomes even more important when cost and technology limitations are issues of concern. Accordingly, a methodology by which one can tailor a sensor **array** to a specific need is highly desirable.
In this paper, a novel method is introduced to address this task using data from an electronic nose that uses polymer gas sensors. This method has been delineated based on the geometry of eigenvectors in Karhunen-Loeve expansion. The methodology is general and therefore suitable for many other feature selection problems.
CLASSIFICATION CODE: 001C01; Chemistry; General chemistry, Physical chemistry
001D02B07B; Applied sciences; Computer science, Software
001D02C; Applied sciences; Artificial intelligence
CONTROLLED TERM: Electronic nose; Karhunen-Loeve expansion; Theory; Sensor data fusion; Data compression; Neural networks; Odors; Chemical sensors

L91 ANSWER 10 OF 18 PASCAL on STN DUPLICATE 8
ACCESSION NUMBER: 1997-0286825 PASCAL
COPYRIGHT NOTICE:
TITLE (IN ENGLISH): Analysis of medication off-odors using an electronic nose
AUTHOR: SCHIFFMAN S. S.; **KERMANI B. G.**; NAGLE H. T.
CORPORATE SOURCE: Department of Psychiatry, Box 3259, Duke University Medical Center, Durham, NC 27710, United States;

Department of Electrical and Computer Engineering, North Carolina State University, Raleigh, NC 27695, United States

SOURCE: Chemical senses, (1997), 22(2), 119-128, refs. 1p. 1/4
ISSN: 0379-864X CODEN: CHSED8

DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United Kingdom
LANGUAGE: English
AVAILABILITY: INIST-16455, 354000065253160020

ABSTRACT: Packaging materials have been implicated as a source for off-odors in pharmaceutical products. A new instrumentation method employing an **array** of conducting polymer gas sensors was used to identify the offending packaging components in the canister of a pharmaceutical inhalant. A case study is described in which tainted inhalers as well as elastomeric components of the canisters were 'sniffed' by the electronic nose. The electronic nose was able to differentiate between tainted and untainted canisters. Signal processing algorithms performed on the raw data from the sensors suggested that specific elastomeric components were responsible for the off-odor. A further experiment suggested that the propellant (Freon) extracted the odor from the elastomeric components as the medication was expelled from the canister. These data indicate that the electronic nose is a potential tool to solve odor problems in which human odor assessment is not feasible due to excess exposure to the medically active ingredient.

CLASSIFICATION CODE: 002B02A03; Life sciences; Medical sciences; Pharmacology
CONTROLLED TERM: Package; Odor; Defect; Measurement method; Instrumentation; Elastomer; Human
BROADER TERM: Perception; Methodology

DUPLICATE 5

ACCESSION NUMBER: 2001:558820 BIOSIS
DOCUMENT NUMBER: PREV200100558820
TITLE: Randomly assembled **arrays** for SNP **genotyping.**

AUTHOR(S): Chee, M. [Reprint author]; Fan, J.-B. [Reprint author]; Wenz, M.; Wickham, E. [Reprint author]; Hayashibara, K.; Chen, J. [Reprint author]; Paner, T.; Doucet, D. [Reprint author]; Zhou, L. [Reprint author]; **Kermani, B.** [Reprint author]; Shen, R. [Reprint author]; Hansen, M. [Reprint author]; Steemers, F. [Reprint author]; Zhao, C. [Reprint author]; Barnard, S. [Reprint author]; Che, D. [Reprint author]; Gunderson, K. [Reprint author]; Barker, D. [Reprint author]; Efcavitch, J.; Oliphant, A. [Reprint author]
CORPORATE SOURCE: Illumina, Inc., San Diego, CA, USA

SOURCE: American Journal of Human Genetics, (October, 2001) Vol. 69, No. 4 Supplement, pp. 516. print.
Meeting Info.: 51st Annual Meeting of the American Society of Human Genetics. San Diego, California, USA. October 12-16, 2001.
CODEN: AJHGAG. ISSN: 0002-9297.

DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)

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LANGUAGE:            English
ENTRY DATE:          Entered STN: 5 Dec 2001
                     Last Updated on STN: 25 Feb 2002
CONCEPT CODE:        General biology - Symposia, transactions and proceedings
                     00520
                     Genetics - General   03502
                     Biochemistry studies - General   10060
                     Biochemistry studies - Nucleic acids, purines and
                     pyrimidines   10062
INDEX TERMS:         Major Concepts
                        Biochemistry and Molecular Biophysics; Genetics; Methods
                        and Techniques
INDEX TERMS:         Chemicals & Biochemicals
                        oligonucleotide
INDEX TERMS:         Methods & Equipment
                        SNP genotyping [single nucleotide polymorphism
                        genotyping]: genetic method
INDEX TERMS:         Miscellaneous Descriptors
                        Meeting Abstract; Meeting Poster

L91  ANSWER 12 OF 18  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation.  on
     STN
ACCESSION NUMBER:    2002:616036  BIOSIS
DOCUMENT NUMBER:     PREV200200616036
TITLE:               A SNP linkage panel genotyped at apprx1,000-plex
                     on randomly assembled arrays.
AUTHOR(S):           Hansen, M. S. T. [Reprint author]; Oliphant, A. [Reprint
                     author]; Fan, J.-B. [Reprint author]; Shen, R. [Reprint
                     author]; Zhou, L. [Reprint author]; Kermani, B.
                     [Reprint author]; Kruglyak, S. [Reprint author]; Dickinson,
                     T. [Reprint author]; Zhao, C. [Reprint author]; Barnard, S.
                     [Reprint author]; Che, D. [Reprint author]; Gunderson, K.
                     [Reprint author]; Barker, D. [Reprint author]; Chee, M. S.
                     [Reprint author]
CORPORATE SOURCE:    Illumina, Inc., San Diego, CA, USA
SOURCE:              American Journal of Human Genetics, (October, 2002) Vol.
                     71, No. 4 Supplement, pp. 204. print.
                     Meeting Info.: 52nd Annual Meeting of the American Society
                     of Human Genetics. Baltimore, MD, USA. October 15-19, 2002.
                     American Society of Human Genetics.
                     CODEN: AJHGAG. ISSN: 0002-9297.
DOCUMENT TYPE:       Conference; (Meeting)
                     Conference; Abstract; (Meeting Abstract)
LANGUAGE:            English
ENTRY DATE:          Entered STN: 4 Dec 2002
                     Last Updated on STN: 4 Dec 2002
CONCEPT CODE:        General biology - Symposia, transactions and proceedings
                     00520
                     Genetics - General   03502
INDEX TERMS:         Major Concepts
                        Genetics; Methods and Techniques
INDEX TERMS:         Methods & Equipment
                        single nucleotide polymorphism assay: genetic
                        method
INDEX TERMS:         Miscellaneous Descriptors
                          genetic map; genotyping; physical
                        map; single nucleotide polymorphism panel; Meeting
                        Abstract

L91  ANSWER 13 OF 18  DISSABS COPYRIGHT (C) 2005 ProQuest Information and
     Learning Company; All Rights Reserved on STN
ACCESSION NUMBER:    96:52587  DISSABS   Order Number: AAR9627637
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TITLE: ON USING ARTIFICIAL NEURAL NETWORKS AND **GENETIC** ALGORITHMS TO OPTIMIZE PERFORMANCE OF AN ELECTRIC NOSE (OLFACTORY)
AUTHOR: **KERMANI, BAHRAM GHAFFARZADEH [PH.D.]**; NAGLE, H. TROY [advisor]
CORPORATE SOURCE: NORTH CAROLINA STATE UNIVERSITY (0155)
SOURCE: Dissertation Abstracts International, (1996) Vol. 57, No. 4B, p. 2754. Order No.: AAR9627637. 213 pages.
DOCUMENT TYPE: Dissertation
FILE SEGMENT: DAI
LANGUAGE: English
ENTRY DATE: Entered STN: 19960903
Last Updated on STN: 19960903

ABSTRACT: In recent years, researchers have tried to mimic the human nose using an **array** of gas sensors in a computer-controlled instrument called the electronic nose (Bartlett and Ling-Chung, 1989; Shurmer et al., 1990b; Chandler and Pletcher, 1985; Gardner et al., 1991b; Heinze, 1990; Miasik et al., 1986; Persaud, 1991; Stetter et al., 1986; Zaromb and Stetter, 1985; Cranny and Atkinson, 1992). Commercial electronic nose systems (AromaScan, 1994; Neotronics, 1994; Alpha MOS, 1994) use **arrays** of gas sensors, with wide sensitivities, to differentiate between various odorants. This differentiation is based on the uniqueness of the data fingerprints of each odorant. A data fingerprint is the accumulative processed response of the **array** of gas sensors. In order to achieve a high recognition rate, it is of paramount importance that the odorprints (fingerprints) be unique and repeatable for each odorant substance. In practice, it has been shown that this uniqueness and repeatability of the data odorprints are difficult to achieve. In reality, the experiments have shown that, for odorants with a small number of volatile molecules such as soft beverages, the current state-of-the-art gas sensor species do not provide useful odorprints. This fact is demonstrated for conducting polymer sensors, which were used in this study. Therefore, a complex signal processing and pattern recognition methodology is needed to overcome the deficit in sensor technology. In this investigation, artificial neural networks have been employed, in conjunction with **genetic** algorithms and traditional signal processing techniques, to perform pattern recognition and data classification. In an attempt to extract more information from the sensor responses, the transient time response of sensors has been used as well as their steady-state values. Several case studies have been performed on a diverse set of families of odorant sources, e.g., coffees, perfumes, soda beverages and hog farm samples. The case studies exhibit promising results in the classification of various substances within each family of odorants. Sophisticated signal processing methods have been shown to be capable of compensating for the deficits in sensor technology.
CLASSIFICATION: 0544 ENGINEERING, ELECTRONICS AND ELECTRICAL; 0541 ENGINEERING, BIOMEDICAL; 0800 ARTIFICIAL INTELLIGENCE

L91 ANSWER 14 OF 18 INSPEC (C) 2005 IEE on STN
ACCESSION NUMBER: 1997:5657282 INSPEC
DOCUMENT NUMBER: A9718-8760J-021; B9709-7510B-250; C9709-7330-269
TITLE: Feature extraction by **genetic** algorithms for neural networks in breast cancer classification.

AUTHOR: **Kermani, B.G.**; White, M.W.; Nagle, H.T.
(Dept. of Electr. & Comput. Eng., North Carolina State Univ., Raleigh, NC, USA)
SOURCE: 1995 IEEE Engineering in Medicine and Biology 17th Annual Conference and 21 Canadian Medical and Biological Engineering Conference (Cat. No.95CH35746) New York, NY, USA: IEEE, 1997. p.831-2 vol.1 of 2 vol. ixviii+1738 pp. 8 refs.
Conference: Montreal, Que., Canada, 20-23 Sept 1995
Price: CCCC 0 7803 2475 7/97/$10.00
ISBN: 0-7803-2475-7
DOCUMENT TYPE: Conference Article
TREATMENT CODE: Practical
COUNTRY: United States
LANGUAGE: English
ABSTRACT: In today's world, in which computerized recognition is expanding its horizons in the field of medicine, breast cancer classification is receiving wide attention. In this application, artificial neural networks have achieved reasonable recognition rates. However, to improve performance, a technique is needed to screen the features of the input data, to extract the important ones and suppress those that are irrelevant. Although neural networks do have this capability to some extent, here it is shown that by using a hybrid **genetic** algorithm and neural network (GANN), the feature extraction can be performed more effectively. Another advantage of augmenting NN training with a GA is that the extracted features using GA are explicit and perceivable. Although the authors evaluated the technique using breast cancer data, the methodology is designed to handle any other kind of classification task.
CLASSIFICATION CODE: A8760J X-rays and particle beams (medical uses); A8770E Patient diagnostic methods and instrumentation; B7510B Radiation and radioactivity applications in biomedicine; B6140C Optical information, image and video signal processing; C7330 Biology and medical computing; C5290 Neural computing techniques; C5260B Computer vision and image processing techniques
CONTROLLED TERM: DIAGNOSTIC RADIOGRAPHY; FEATURE EXTRACTION; **GENETIC** ALGORITHMS; IMAGE CLASSIFICATION; MEDICAL IMAGE PROCESSING; NEURAL NETS
SUPPLEMENTARY TERM: **genetic algorithm feature extraction**; breast cancer classification; computerized recognition; input data features screening; **hybrid genetic algorithm**; important data extraction; irrelevant data suppression; X-ray images; medical diagnostic imaging
ELEMENT TERM: In

L91 ANSWER 15 OF 18 COMPENDEX COPYRIGHT 2005 EEI on STN
ACCESSION NUMBER: 1997(20):4137 COMPENDEX
TITLE: Feature extraction by **genetic** algorithms for neural networks in breast cancer classification.
AUTHOR: **Kermani, Bahram G.** (North Carolina State Univ, Raleigh, NC, USA); White, Mark W.; Nagle, H.Troy
MEETING TITLE: Proceedings of the 1995 IEEE Engineering in Medicine and Biology 17th Annual Conference and 21st Canadian Medical and Biological Engineering Conference.
MEETING ORGANIZER: IEEE
MEETING LOCATION: Montreal, Can

MEETING DATE: 20 Sep 1995-23 Sep 1995
SOURCE: Annual International Conference of the IEEE Engineering in Medicine and Biology - Proceedings v 17 n 1 1995.,95CB35746.p 831-832
CODEN: CEMBAD ISSN: 0589-1019
PUBLICATION YEAR: 1995
MEETING NUMBER: 46181
DOCUMENT TYPE: Conference Article
TREATMENT CODE: Application
LANGUAGE: English
ABSTRACT: In today's world, in which computerized recognition is expanding its horizons in the field of medicine, breast cancer classification is receiving wide attention. In this application, artificial neural networks have achieved reasonable recognition rates left bracket 1,2 right bracket .However, to improve performance, a technique is needed to screen the features of the input data, to extract the important ones and suppress those that are irrelevant. Although neural networks do have this capability to some extent, in this paper it is shown that by using a hybrid **Genetic** Algorithm and Neural Network (GANN), the feature extraction can be performed more effectively. Another advantage of augmenting NN training with a GA is that the extracted features using GA are explicit and perceivable. Although we evaluated the technique using breast cancer data left bracket 3 right bracket , the methodology is designed to handle any other kind of classification task.(Author abstract) 8 Refs.
CLASSIFICATION CODE: 723.4 Artificial Intelligence; 461.2 Biological Materials; 723.2 Data Processing
CONTROLLED TERM: *Neural networks; Oncogenic viruses; Feature extraction; Performance; Backpropagation; **Genetic** algorithms; Pattern recognition
SUPPLEMENTARY TERM: Breast cancer classification; Breast cancer; Radial basis; Feature selection

L91 ANSWER 16 OF 18 COMPUAB
ACCESSION NUMBER: 1999:5664 COMPUAB
DOCUMENT NUMBER: 395584 (CI)
TITLE: Using neural networks and **genetic** algorithms to enhance performance in an electronic nose
AUTHOR: **Kermani B G**; Schiffman S S; Nagle H T
CORPORATE SOURCE: Lucent Technologies, Allentown, PA, USA.
SOURCE: IEEE Transactions on Biomedical Engineering, Vol. 46, No. 4 , pp. 429-439, 19990000. Publisher: Institute of Electrical and Electronics Engineers, Inc , 445Hoes Ln, Piscataway, NJ, 08854-1331, UK, [mailto:inspec@ieee.org].
ISSN: 0018-9294.
DOCUMENT TYPE: Journal
FILE SEGMENT: Computer & Information Systems
LANGUAGE: English
ENTRY DATE: Entered STN: 20041219
Last Updated on STN: 20041219
ABSTRACT: Sensitivity, repeatability, and discernment are three major issues in any classification problem. In this study, an electronic nose with an **array** of 32 sensors was used to classify a range of odorous substances. The collective time response of the sensor **array** was first partitioned into four time segments, using four

smooth time-windowing functions. The dimension of the data associated with each time segment was then reduced by applying the Karhunen-Loeve (truncated) expansion (KLE). An ensemble of the reduced data patterns was then used to train a neural network (NN) using the Levenberg-Marquardt (LM) learning method. A **genetic** algorithm (GA)-based evolutionary computation method was used to devise the appropriate NN training parameters, as well as the effective database partitions/features. Finally, it was shown that a GA-supervised NN system (GANN) outperforms the NN-only classifier, for the classes of the odorants investigated in this study (fragrances, hog farm air, and soft beverages).

CLASSIFICATION: W4 723.4 Artificial Intelligence; C 723.4 Artificial Intelligence; W4 461.4 Human Engineering; W4 723.5 Computer Applications; W4 723.2 Data Processing; C 461.4 Human Engineering; C 723.5 Computer Applications; C 723.2 Data Processing (CI)

UNCONTROLLED TERM: **Genetic** Algorithms; Sensory Perception; Artificial Intelligence; Pattern Recognition; Digital Signal Processing

L91 ANSWER 17 OF 18 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation. on STN

ACCESSION NUMBER: 2003:347429 SCISEARCH
THE GENUINE ARTICLE: 594AC
TITLE: A SNP linkage panel **genotyped** at similar to 1,000-plex on randomly assembled **arrays.**
AUTHOR: Hansen M S T (Reprint); Oliphant A; Fan J B; Shen R; Zhou L; **Kermani B**; Kruglyak S; Dickinson T; Zhao C; Barnard S; Che D; Gunderson K; Barker D; Chee M S
CORPORATE SOURCE: Illumina Inc, San Diego, CA USA
COUNTRY OF AUTHOR: USA
SOURCE: AMERICAN JOURNAL OF HUMAN GENETICS, (OCT 2002) Vol. 71, No. 4, Supp. [S], pp. 204-204. MA 203.
Publisher: UNIV CHICAGO PRESS, 1427 E 60TH ST, CHICAGO, IL 60637-2954 USA.
ISSN: 0002-9297.
DOCUMENT TYPE: Conference; Journal
LANGUAGE: English
REFERENCE COUNT: 0
CATEGORY: GENETICS & HEREDITY

L91 ANSWER 18 OF 18 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2000-533047 [48] WPIDS
CROSS REFERENCE: 2002-196268 [25]
DOC. NO. NON-CPI: N2000-394270
DOC. NO. CPI: C2000-158878
TITLE: **Array** of microspheres, useful e.g. for detecting specific analytes, includes fiducial components to allow computerized comparison of data images from the **array.**
DERWENT CLASS: B04 D16 J04 S03
INVENTOR(S): BREZNER, D J; CHEE, M S; DICKINSON, T A; GUNDERSON, K; STUELPNAGEL, J R; HAAS, J; **KERMANI, B G**
PATENT ASSIGNEE(S): (ILLU-N) ILLUMINA INC; (CHEE-I) CHEE M S; (DICK-I) DICKINSON T A; (HAAS-I) HAAS J; (KERM-I) KERMANI B G; (STUE-I) STUELPNAGEL J R
COUNTRY COUNT: 90
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC

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WO 2000047996   A2 20000817 (200048)* EN   49 G01N033-50
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       OA PT SD SE SL SZ TZ UG ZW
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       FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS
       LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ
       TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2000033594   A  20000829 (200062)          G01N033-50
EP 1206315      A2 20020522 (200241)  EN      B01J019-00
    R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
       RO SE SI
US 2002150909   A1 20021017 (200270)          C12Q001-68
JP 2002536665   W  20021029 (200274)       71 G01N033-53
AU 771458       B2 20040325 (200454)          G01N033-50
CA 2359352      C  20040921 (200463)  EN      B01J019-00
AU 2004202799   A1 20040722 (200471)#         G01N033-50
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APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
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AU 2000033594	A	AU 2000-33594	20000209
EP 1206315	A2	EP 2000-911745	20000209
		WO 2000-US3375	20000209
US 2002150909	A1 Provisional	US 1999-119323P	19990209
	CIP of	US 2000-500555	20000209
	CIP of	US 2000-636387	20000809
		US 2001-925941	20010809
JP 2002536665	W	JP 2000-598854	20000209
		WO 2000-US3375	20000209
AU 771458	B2	AU 2000-33594	20000209
CA 2359352	C	CA 2000-2359352	20000209
		WO 2000-US3375	20000209
AU 2004202799	A1	AU 2004-202799	20040623

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000033594	A Based on	WO 2000047996
EP 1206315	A2 Based on	WO 2000047996
JP 2002536665	W Based on	WO 2000047996
AU 771458	B2 Previous Publ.	AU 2000033594
	Based on	WO 2000047996
CA 2359352	C Based on	WO 2000047996
AU 2004202799	A1 Div ex	AU 771458

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PRIORITY APPLN. INFO: US 1999-119323P     19990209; US
                      2000-500555       20000209; US
                      2000-636387       20000809; US
                      2001-925941       20010809; AU
                      2004-202799       20040623
INT. PATENT CLASSIF.:
          MAIN:       B01J019-00; C12Q001-68; G01N033-50; G01N033-53
     SECONDARY:       C07H021-04; G01N021-64; G01N021-77; G01N021-78;
                      G01N033-48; G01N033-566; G01N037-00; G06F019-00;
                      G06K009-00; G06T007-00
```

BASIC ABSTRACT:

WO 200047996 A UPAB: 20041104

NOVELTY - **Array** composition (A) comprising a substrate (S) with

discrete sites on its surface, at least 2 subpopulations of microspheres (MS), each subpopulation including a bioactive agent (I), distributed over the surface of S, and at least 1 fiducial (F, i.e. a physical reference feature that allows precise comparison of sequential data images of the **array**), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(a) system (B) comprising a computer-readable memory, for controlling a computer, consisting of modules for:

(i) recording a data image from a random **array** of discrete sites;

(ii) registering data images; and

(iii) comparing registered images;

(b) making (A) comprising forming a surface with individual sites on a substrate, distributing MS over the surface, and at least 1 F is incorporated into the surface

(c) computer-based comparison of separate data images of a random **array**;

(d) decoding a random **array** comprising treating an **array** (substrate plus MS) with many decoder binding ligands (DBLs) to create a data image, using F used to generate a registered data image, applying a second mixture of DBL and generating a second registered data image and comparing the images by computer to identify the locations of at least 2 (I); and

(e) determining presence of a target analyte (II) in a sample by comparing data images from an **array** as in (f), where the first and second images are registered before and after treatment of the **array** with a test sample.

USE - (A) is used to detect and quantify selected analytes (II), e.g. pollutants, therapeutic drugs, antigens, viruses, etc. particularly proteins and nucleic acids. Typical applications are in genetic diagnosis (e.g. of genes or mutations associated with cancer or Alzheimer's disease), screening blood for bacteria and viruses, monitoring of therapy, forensic DNA fingerprinting, and nucleic acid sequencing by hybridization. (A) are also useful in screening to identify agents that bind to, and preferably modify function of, a target molecule.

ADVANTAGE - The presence of F permits comparison of sequential images of (A), by preserving the relative positions of each site within the **array.** The synthesis and positioning of (I) can now be done separately, and the (I)-loaded MS can be distributed randomly, which is quicker and less expensive than in situ synthesis or spotting techniques. By using fiber optical techniques, **arrays** of very high density may be produced, e.g. about 25 million beads and fibers per 0.5 square cm. For quality control or calibration, the performance of every probe in every **array** can be tested by decoding with specific ligands.

Dwg.0/2

FILE SEGMENT: CPI EPI
FIELD AVAILABILITY: AB; DCN
MANUAL CODES: CPI: B04-B04D5; B04-E05; B04-N04; B11-C07A; B11-C08E; B11-C08E5; B12-K04A; B12-K04A4; B12-K04E; B12-K04F; D05-H09; D05-H12D1; J04-B01
EPI: S03-E14H

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USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE COVERS 1907 - 23 Feb 2005  VOL 142 ISS 9
FILE LAST UPDATED: 22 Feb 2005  (20050222/ED)

  This file contains CAS Registry Numbers for easy and accurate
  substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

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L5         58029 SEA FILE=CAPLUS ABB=ON  ARRAY?/OBI OR MICROARRAY?/OBI
L8             1 SEA FILE=CAPLUS ABB=ON  (SWEEP POINT#)/BI
L10            8 SEA FILE=CAPLUS ABB=ON  (REGISTRATION#(2A)TRANSFORM?)/BI
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L13          237 SEA FILE=CAPLUS ABB=ON  DELAUNAY/BI
L15            0 SEA FILE=CAPLUS ABB=ON  L12 AND L13 AND (L2 OR L3 OR L4 OR L5)



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L23            0 SEA FILE=CAPLUS ABB=ON  L7 AND L9

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L6          5097 SEA FILE=CAPLUS ABB=ON  NORMALIZ?/OBI
L17            3 SEA FILE=CAPLUS ABB=ON  L2 AND L6
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L4         42048 SEA FILE=CAPLUS ABB=ON  GENOTYP?/OBI
L6          5097 SEA FILE=CAPLUS ABB=ON  NORMALIZ?/OBI
L18           16 SEA FILE=CAPLUS ABB=ON  (L3 OR L4) AND L6
L19            4 SEA FILE=CAPLUS ABB=ON  L18 AND DNA/TI


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                 L7 OR L8 OR L9 OR L10)


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L92            9 L17 OR L19 OR L24 OR L33

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MOST RECENT DERWENT UPDATE:      200512         <200512/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

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    GUIDES, PLEASE VISIT:
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    DOCUMENTATION NOW AVAILABLE IN DERWENT WORLD PATENTS INDEX
    FIRST VIEW - FILE WPIFV.
    FOR FURTHER DETAILS: http://www.thomsonderwent.com/dwpifv  <<<
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>>> SMILES and ISOSMILES strings are no longer available as
    Derwent Chemistry Resource display fields  <<<

>>> THE CPI AND EPI MANUAL CODES HAVE BEEN REVISED FROM UPDATE 200501.
    PLEASE CHECK:
http://thomsonderwent.com/support/dwpiref/reftools/classification/code-revision/
    FOR DETAILS. <<<

=> d que l52; d que l57

L35         3564 SEA FILE=WPIDS ABB=ON  ALLELE#
L36         2764 SEA FILE=WPIDS ABB=ON  GENOTYP?
L38         3468 SEA FILE=WPIDS ABB=ON  MICROARRAY#
L41           15 SEA FILE=WPIDS ABB=ON  SWEEP POINT#
L43          581 SEA FILE=WPIDS ABB=ON  (REGISTRATION OR CONFORMATION? OR
                PROJECT?)(3A)TRANSFORM?
L44           31 SEA FILE=WPIDS ABB=ON  DELAUNAY
L46           49 SEA FILE=WPIDS ABB=ON  GENETIC DATA#
L52            0 SEA FILE=WPIDS ABB=ON  (L35 OR L36 OR L38 OR L46) AND (L41 OR
                L43 OR L44)



L39        15854 SEA FILE=WPIDS ABB=ON  NORMALI?
L46           49 SEA FILE=WPIDS ABB=ON  GENETIC DATA#
L57            0 SEA FILE=WPIDS ABB=ON  L46 AND L39


=> d que l54; d que l58; d que l59

L44           31 SEA FILE=WPIDS ABB=ON  DELAUNAY
L45         1584 SEA FILE=WPIDS ABB=ON  TRIANGULAT?
L53           13 SEA FILE=WPIDS ABB=ON  L44 AND L45
L54            2 SEA FILE=WPIDS ABB=ON  L53 AND MOLECUL?/TI



L35         3564 SEA FILE=WPIDS ABB=ON  ALLELE#
L36         2764 SEA FILE=WPIDS ABB=ON  GENOTYP?
L37       156518 SEA FILE=WPIDS ABB=ON  ARRAY#
L38         3468 SEA FILE=WPIDS ABB=ON  MICROARRAY#
L40         7980 SEA FILE=WPIDS ABB=ON  (COORDINATE OR CO ORDINATE)(2A)SYSTEM#
L41           15 SEA FILE=WPIDS ABB=ON  SWEEP POINT#
L43          581 SEA FILE=WPIDS ABB=ON  (REGISTRATION OR CONFORMATION? OR
                PROJECT?)(3A)TRANSFORM?
L44           31 SEA FILE=WPIDS ABB=ON  DELAUNAY
L46           49 SEA FILE=WPIDS ABB=ON  GENETIC DATA#
L49           29 SEA FILE=WPIDS ABB=ON  ((L35 OR L36 OR L37 OR L38) OR L46) AND
                (L41 OR L43 OR L44)
L56           18 SEA FILE=WPIDS ABB=ON  L40 AND L43
L58            1 SEA FILE=WPIDS ABB=ON  L56 AND ((L35 OR L36 OR L37 OR L38) OR
                L49)



L42         3946 SEA FILE=WPIDS ABB=ON  CONTROL POINT#
L43          581 SEA FILE=WPIDS ABB=ON  (REGISTRATION OR CONFORMATION? OR
                PROJECT?)(3A)TRANSFORM?
L59            2 SEA FILE=WPIDS ABB=ON  L42 AND L43
```

=> s l54 or l58 or l59

L93 5 L54 OR L58 OR L59

=> fil JICST-EPLUS, PASCAL, BIOTECHNO, ESBIOBASE, BIOSIS, DISSABS, JAPIO, INSPEC, COMPENDEX, COMPUSCIENCE, COMPUAB, SCISEARCH

FILE 'JICST-EPLUS' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'PASCAL' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'BIOTECHNO' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'ESBIOBASE' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'BIOSIS' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'DISSABS' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'JAPIO' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'INSPEC' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'COMPENDEX' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'COMPUSCIENCE' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'COMPUAB' ENTERED AT 12:26:16 ON 23 FEB 2005

FILE 'SCISEARCH' ENTERED AT 12:26:16 ON 23 FEB 2005

=> d que l78; d que l77; d que l82

L62	315958	SEA ALLELE#
L63	367676	SEA GENOTYP?
L64	1845597	SEA GENETIC
L65	691272	SEA ARRAY#
L66	55463	SEA MICROARRAY#
L67	302708	SEA NORMALIZ? OR NORMALIS?
L68	41265	SEA (COORDINATE OR CO ORDINATE)(W) SYSTEM#
L69	19	SEA SWEEP POINT#
L70	16525	SEA CONTROL POINT#

```
L71          5953 SEA DELAUNAY
L72         30643 SEA TRIANGULAT?
L73          6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?)(3A) TRANSFORM?
L78             0 SEA L69 AND ((L62 OR L63 OR L64 OR L65 OR L66 OR L67 OR L68)
                  OR (L70 OR L71 OR L72 OR L73))



L62        315958 SEA ALLELE#
L63        367676 SEA GENOTYP?
L64       1845597 SEA GENETIC
L67        302708 SEA NORMALIZ? OR NORMALIS?
L68         41265 SEA (COORDINATE OR CO ORDINATE)(W) SYSTEM#
L76          7433 SEA L67 AND (L62 OR L63 OR L64)
L77             0 SEA L76 AND L68



L62        315958 SEA ALLELE#
L63        367676 SEA GENOTYP?
L64       1845597 SEA GENETIC
L67        302708 SEA NORMALIZ? OR NORMALIS?
L68         41265 SEA (COORDINATE OR CO ORDINATE)(W) SYSTEM#
L70         16525 SEA CONTROL POINT#
L71          5953 SEA DELAUNAY
L72         30643 SEA TRIANGULAT?
L73          6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?)(3A) TRANSFORM?
L79            30 SEA L71 AND L72 AND (L62 OR L63 OR L64)
L82             0 SEA L79 AND (L68 OR L70 OR L73 OR L67)

=> d que l83; d que l85; d que l90

L62        315958 SEA ALLELE#
L63        367676 SEA GENOTYP?
L64       1845597 SEA GENETIC
L65        691272 SEA ARRAY#
L66         55463 SEA MICROARRAY#
L71          5953 SEA DELAUNAY
L72         30643 SEA TRIANGULAT?
L79            30 SEA L71 AND L72 AND (L62 OR L63 OR L64)
L83             2 SEA L79 AND (L65 OR L66)



L62        315958 SEA ALLELE#
L63        367676 SEA GENOTYP?
L64       1845597 SEA GENETIC
L71          5953 SEA DELAUNAY
L72         30643 SEA TRIANGULAT?
L85            19 SEA L71(L) L72(L) (L62 OR L63 OR L64)



L62        315958 SEA ALLELE#
L63        367676 SEA GENOTYP?
L64       1845597 SEA GENETIC
L65        691272 SEA ARRAY#
L66         55463 SEA MICROARRAY#
L67        302708 SEA NORMALIZ? OR NORMALIS?
L68         41265 SEA (COORDINATE OR CO ORDINATE)(W) SYSTEM#
L70         16525 SEA CONTROL POINT#
```

```
L71         5953 SEA DELAUNAY
L72        30643 SEA TRIANGULAT?
L73         6608 SEA (REGIST? OR CONFORMATION? OR PROJECT?)(3A) TRANSFORM?
L89          160 SEA (L62 OR L63 OR L64) AND L68
L90            7 SEA L89 AND ((L65 OR L66 OR L67) OR (L70 OR L71 OR L72 OR
               L73))

=> s l83 or l85 or l90

L94           26 L83 OR L85 OR L90

=> => dup rem l92,l94,l93
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PROCESSING COMPLETED FOR L92
PROCESSING COMPLETED FOR L94
PROCESSING COMPLETED FOR L93
L95           31 DUP REM L92 L94 L93 (9 DUPLICATES REMOVED)
                 ANSWERS '1-9' FROM FILE CAPLUS
                 ANSWERS '10-12' FROM FILE JICST-EPLUS
                 ANSWERS '13-15' FROM FILE PASCAL
                 ANSWER '16' FROM FILE ESBIOBASE
                 ANSWERS '17-25' FROM FILE INSPEC
                 ANSWER '26' FROM FILE COMPUSCIENCE
                 ANSWERS '27-31' FROM FILE WPIDS

=> d ibib ed abs hitind 1-9; d iall 10-31; fil hom

L95  ANSWER 1 OF 31  CAPLUS  COPYRIGHT 2005 ACS on STN
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ACCESSION NUMBER: 2005:14597 CAPLUS
DOCUMENT NUMBER: 142:108376
TITLE: Mutation/polymorphism analysis by **DNA** microarray with matching and mismatching probes and signal correction
INVENTOR(S): Nagaoka, Tomonori
PATENT ASSIGNEE(S): Olympus Corporation, Japan
SOURCE: PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005001125	A1	20050106	WO 2004-JP9275	20040624

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: JP 2003-184474 A 20030627

ED Entered STN: 07 Jan 2005

AB Provide a means of, in analyzing mutations or polymorphisms with the use of a DNA microarray, identifying whether a signal from each of spots on the DNA microarray perfectly or imperfectly matches between a probe and a target nucleic acid, even in the case of using a sample nucleic acid mol. having a hetero (heterozygous/heterogeneous) sequence. A method is characterized by using a sample exclusively having candidates for a perfectly matching probe and a perfectly matching nucleic acid, subtracting the signal data thus obtained from untreated data to thereby correct signal values caused by nonspecific hybridization, and, in the case where the corrected signal value amts. to a certain level or higher, identifying the signal as originating in perfect matching. A rapid, precise, and accurate microarray-based method has been developed that uses a signal data normalization for detection of mutations. Authors used the DNA microarray to detect mutations in codon 12 of K-ras. Fluorescein isothiocyanate-labeled PCR products were analyzed with the microarray. Authors could correctly identify wild-type, heterozygous, and homozygous mutant genotypes with the DNA microarray in <3.5 h. This is a novel DNA microarray system and can be used to analyze K-ras mutations quickly and accurately.

IC ICM C12Q001-68
ICS C12N015-09; C12M001-00; G01N033-53; G01N033-566; G01N037-00

CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9

ST mutation polymorphism DNA microarray analysis matching mismatching probe; signal **normalization** data correction DNA microarray mutation polymorphism

IT DNA microarray technology
Genetic polymorphism
Genotyping (method)
Mutation
(mutation/polymorphism anal. by DNA microarray with matching and mismatching probes and signal correction)

IT Data processing
(**normalization**; mutation/polymorphism anal. by DNA microarray with matching and mismatching probes and signal correction)
REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 2 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:27135 CAPLUS
DOCUMENT NUMBER: 140:289452
TITLE: Process design optimisation using embedded hybrid visualization and **data** analysis techniques within a **genetic** algorithm optimisation framework
AUTHOR(S): Wang, K.; Salhi, A.; Fraga, E. S.
CORPORATE SOURCE: Centre for Process Systems Engineering, Department of Chemical Engineering, University College London (UCL), London, WC1E 7JE, UK
SOURCE: Chemical Engineering and Processing (2004), 43(5), 657-669
CODEN: CENPEU; ISSN: 0255-2701
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 13 Jan 2004
AB Process optimization is a difficult task due to the non-linear, non-convex and often discontinuous nature of the math. models used. Although significant advances in deterministic methods were made, stochastic procedures, specifically genetic algorithms, provide an attractive technol. for solving these optimization problems. However, genetic algorithms are not naturally suited to highly constrained problems. We propose a targeted genetic algorithm for process optimization which is suitable for highly constrained problems. The genetic operators, crossover and mutation, are defined based on information gained about the feasible region and the behavior of the objective function through the use of a data anal. procedure. The data anal. is based on a visual representation, the parallel **coordinate system.** A pattern matching algorithm, the Scan Circle Algorithm [K. Wang, A. Salhi, E.S. Fraga, Cluster identification using a parallel **coordinate system** for knowledge discovery and nonlinear optimization, in: J. Grievink, J. van Schijndel (Eds.), Proceedings of the 12th European Symposium on Computer-Aided Process Engineering, Computer-Aided Chemical Engineering, volume 10, Elsevier, Amsterdam, 2002, pp. 1003-1008], is extended through the use of Learning Vector Quantization [T. Kohonen, Self-Organizing Maps, Springer-Verlag, Heidelberg, 1995] to identify, automatically, key features of the objective function and the search space. These features are used to target the genetic operators. Results from the application of the new targeted genetic algorithm to an oil stabilization problem are presented, demonstrating the effective, efficient and robust nature of the implementation. The use of visualization as the core of the data anal. step also provides a useful tool for explaining the results obtained by the optimization procedure.
CC 48-10 (Unit Operations and Processes)
ST design optimization visualization **data genetic** algorithm
IT Algorithm
(**genetic**; process design optimization using embedded hybrid visualization and **data** anal. techniques within **genetic** algorithm optimization framework)
IT Optimization
(nonlinear; process design optimization using embedded hybrid visualization and **data** anal. techniques within **genetic** algorithm optimization framework)

IT Chemical engineering design
(process design optimization using embedded hybrid visualization and **data** anal. techniques within **genetic** algorithm optimization framework)
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 3 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:407896 CAPLUS
DOCUMENT NUMBER: 141:119618
TITLE: Fast automatic registration of images using the phase of a complex wavelet transform: application to proteome gels
AUTHOR(S): Woodward, Andrew M.; Rowland, Jem J.; Kell, Douglas B.
CORPORATE SOURCE: Institute of Biological Sciences, University of Wales, Aberystwyth, SY23 3DD, UK
SOURCE: Analyst (Cambridge, United Kingdom) (2004), 129(6), 542-552
CODEN: ANALAO; ISSN: 0003-2654
PUBLISHER: Royal Society of Chemistry
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 20 May 2004
AB Image registration describes the process of manipulating a distorted version of an image such that its pixels overlay the equivalent pixels in a clean, master or reference image. The need for it has assumed particular prominence in the anal. of images of electrophoretic gels used in the anal. of protein expression levels in living cells, but also has fundamental applications in most other areas of image anal. Much of the positional information of a data feature is carried in the phase of a complex transform, so a complex transform allows explicit specification of the phase, and hence of the position of features in the image. Registration of a test gel to a reference gel is achieved by using a multiresoln. movement map derived from the phase of a complex wavelet transform (the Q-shift wavelet transform) to dictate the warping directly via movement of the nodes of a **Delaunay-triangulated** mesh of points. This warping map is then applied to the original untransformed image such that the absolute magnitude of the spots remains unchanged. The technique is general to any type of image. Results are presented for a simple computer simulated gel, a simple real gel registration between similar "clean" gels with local warping vectors distributed about one main direction, a hard problem between a reference gel and a "dirty" test gel with multi-directional warping vectors and many artifacts, and some typical gels of present interest in post-genomic biol. The method compares favorably with others, since it is computationally rapid, effective and entirely automatic.
CC 9-7 (Biochemical Methods)
Section cross-reference(s): 6, 10
ST protein QSWT automatic **registration** wavelet **transform** proteome gel electrophoresis
IT Algorithm
(DTWT (dual tree wavelet complex **transform**); fast automatic **registration** of images using the phase of complex wavelet transform for proteome 2-D gels)
IT Algorithm
(QSWT (Q-shift **transform**); fast automatic **registration** of images using the phase of complex wavelet transform for proteome 2-D gels)
REFERENCE COUNT: 95 THERE ARE 95 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 4 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2003:686485 CAPLUS
DOCUMENT NUMBER: 139:318111
TITLE: Quantification of single nucleotide polymorphisms by automated **DNA** sequencing
AUTHOR(S): Qiu, Ping; Soder, George J.; Sanfiorenzo, Vincent J.; Wang, Luquan; Greene, Jonathan R.; Fritz, Mary Ann; Cai, Xiao-Yan
CORPORATE SOURCE: Bioinformatics Group and Discovery Technology Department, Schering-Plough Research Institute, Kenilworth, NJ, 07033, USA
SOURCE: Biochemical and Biophysical Research Communications (2003), 309(2), 331-338
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 03 Sep 2003
AB Single nucleotide polymorphisms (SNPs) are linked to phenotypes associated with diseases and drug responses. Many techniques are now available to identify and quantify such SNPs in DNA or RNA pools, although the information on the latter is limited. The majority of these methodologies require prior knowledge of target sequences, normally obtained through DNA sequencing. Direct quantitation of SNPs from DNA sequencing raw data will save time and money for large amount sample anal. A high throughput DNA sequencing assay, in combination with a SNP quant. algorithm, was developed for the quantitation of a SNP present in HCV RNA sequences. For a side-by-side comparison, a Pyrosequencing assay was also developed. Quantitation performance was evaluated for both methods. The direct DNA sequencing quantitation method was shown to be more linear, accurate, sensitive, and reproducible than the Pyrosequencing method for the quantitation of the SNP present in HCV RNA mols.
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 10
IT **Genotypes**
(heterozygosity, quantitation of; quantification of single nucleotide polymorphisms by automated DNA sequencing)
IT Algorithm
(**normalize** peak height, report background level, quantify heterozygous bases; quantification of single nucleotide polymorphisms by automated DNA sequencing)
REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 5 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:250454 CAPLUS
DOCUMENT NUMBER: 137:120237
TITLE: **Normalization** of cDNA microarray data using exogenous nucleic acid control in gene differential expression determination
AUTHOR(S): Zhang, Liang; Zhang, Jian; Zhou, Yu-xiang; Cheng, Jing
CORPORATE SOURCE: Department of Biological Science and Technology, Tsinghua University, Beijing, 100084, Peop. Rep. China
SOURCE: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao (2002), 18(1), 115-119
CODEN: ZSHXF2; ISSN: 1007-7626
PUBLISHER: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao Bianweihui
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
ED Entered STN: 04 Apr 2002
AB In DNA microarray technol., it is necessary to determine the detection sensitivity level and normalize the difference in Dye incorporation and

quantum yield. In the past, the housekeeping genes were frequently used to normalize the microarray data. However, more recent reports indicate that the expression levels of housekeeping genes can vary. Three exogenous polyadenylated RNA were produced through in vitro transcription and used as internal control RNA, standing for high, medium and low abundance resp. The result showed that the fluorescent signal intensity of hybridization was pos. correlative with the gene transcript abundance and gene differential expression was identified in both DNA microarray and Northern blot methods.

CC 3-1 (Biochemical Genetics)

IT Gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression; **normalization** of cDNA microarray data using exogenous nucleic acid control in gene differential expression determination)

IT DNA microarray technology
Transcription, **genetic**
(**normalization** of cDNA microarray **data** using exogenous nucleic acid control in gene differential expression determination)

IT RNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(poly(A)-containing; **normalization** of cDNA microarray data using exogenous nucleic acid control in gene differential expression determination)

L95 ANSWER 6 OF 31 CAPLUS

ACCESSION NUMBER: 2002:565465 CAPLUS
DOCUMENT NUMBER: 138:52111
TITLE: Knowledge-based image processing for on-off type **DNA** microarray
AUTHOR(S): Kim, Jong Dae; Kim, Seo Kyu; Cho, Jeong Sik; Kim, Jongwon
CORPORATE SOURCE: Div. of Inform. and Comm. Eng., Hallym University, Chunchon, S. Korea
SOURCE: Proceedings of SPIE-The International Society for Optical Engineering (2002), 4623(Functional Monitoring and Drug-Tissue Interaction), 38-46
CODEN: PSISDG; ISSN: 0277-786X
PUBLISHER: SPIE-The International Society for Optical Engineering
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 31 Jul 2002

AB This paper addresses the image processing technique for discriminating whether the probes are hybridized with target DNA in the Human Papilloma Virus (HPV) DNA Chip designed for genotyping HPV. In addition to the probes, the HPV DNA chip has markers that always react with the sample DNA. The positions of probe-dots in the final scanned image are fixed relative to the marker-dot locations with a small variation according to the accuracy of the dotter and the scanner. The probes are duplicated 4 times for the diagnostic stability. The prior knowledges such as the maker relative distance and the duplication information of probes is integrated into the template matching technique with the normalized correlation measure. Results show that the employment of both of the prior knowledges is to simply average the template matching measures over the positions of the markers and probes. The eventual proposed scheme yields stable marker locating and probe classification.

CC 9-1 (Biochemical Methods)
Section cross-reference(s): 3, 20

IT Human papillomavirus
(HPV, DNA Chip **genotyping**; knowledge-based image processing for on-off type HPV DNA microarray)

IT Statistical analysis
(**normalized** correlation, for marker locating and probe classification; knowledge-based image processing for on-off type HPV

DNA microarray)
REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 7 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:597001 CAPLUS
DOCUMENT NUMBER: 138:101428
TITLE: Accurate **normalization** of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes
AUTHOR(S): Vandesompele, Jo; De Preter, Katleen; Pattyn, Filip; Poppe, Bruce; Van Roy, Nadine; De Paepe, Anne; Speleman, Frank
CORPORATE SOURCE: Center for Medical Genetics, Ghent University Hospital 1K5, Ghent, B-9000, Belg.
SOURCE: GenomeBiology [online computer file] (2002), 3(7), No pp. given
CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/2002/3/7/research/0034.1
PUBLISHER: BioMed Central Ltd.
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English
ED Entered STN: 12 Aug 2002
AB Background: Gene-expression anal. is increasingly important in biol. research, with real-time reverse transcription PCR (RT-PCR) becoming the method of choice for high-throughput and accurate expression profiling of selected genes. Given the increased sensitivity, reproducibility and large dynamic range of this methodol., the requirements for a proper internal control gene for normalization have become increasingly stringent. Although housekeeping gene expression has been reported to vary considerably, no systematic survey has properly determined the errors related to the common practice of using only one control gene, nor presented an adequate way of working around this problem. Results: We outline a robust and innovative strategy to identify the most stably expressed control genes in a given set of tissues, and to determine the min. number of genes required to calculate a reliable normalization factor. We have evaluated ten housekeeping genes from different abundance and functional classes in various human tissues, and demonstrated that the conventional use of a single gene for normalization leads to relatively large errors in a significant proportion of samples tested. The geometric mean of multiple carefully selected housekeeping genes was validated as an accurate normalization factor by analyzing publicly available microarray data. Conclusions: The normalization strategy presented here is a prerequisite for accurate RT-PCR expression profiling, which, among other things, opens up the possibility of studying the biol. relevance of small expression differences.
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 6, 7, 13
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(14-3-3, zeta subunit, use as internal housekeeping gene control of gene YWHAZ for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT Ribosomal proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(L13a, use as internal housekeeping gene control of gene RPL13A for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT PCR (polymerase chain reaction)
(RT-PCR (reverse transcription-PCR), real-time quant.; accurate **normalization** of real-time quant. RT-PCR data by geometric

averaging of multiple internal control genes)
IT Human
(RT-PCR for human gene targets; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(TBP (TATA box-binding protein), use as internal housekeeping gene control of gene TBP for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT Primers (nucleic acid)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(for internal housekeeping gene controls in RT-PCR; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT **Genetic** methods
(gene expression profiling by RT-PCR; accurate **normalization** of real-time quant. RT-PCR **data** by geometric averaging of multiple internal control genes)
IT Gene, animal
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(housekeeping genes; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT Gene expression profiles, animal
(of housekeeping genes; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal control genes)
IT Actins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(β-, use as internal housekeeping gene control of gene ACTB for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT Microglobulins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(β2-, use as internal housekeeping gene control of gene B2M for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT 9016-12-0, Hypoxanthine phosphoribosyl transferase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(I, use as internal housekeeping gene control of gene HPRT1 for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT 485877-14-3 485877-15-4 485877-16-5 485877-17-6 485877-18-7
485877-19-8 485877-20-1 485877-21-2 485877-22-3 485877-23-4
485877-24-5 485877-25-6 485877-26-7 485877-27-8 485877-28-9
485877-29-0 485877-30-3 485877-31-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(PCR primer; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT 9002-02-2, Succinate dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(subunit A, use as internal housekeeping gene control of gene SDHA for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)
IT 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(use as internal housekeeping gene control of gene GAPD for; accurate

normalization of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)

IT 9074-91-3, Hydroxymethyl-bilane synthase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(use as internal housekeeping gene control of gene HMBS for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)

IT 151821-62-4, Ubiquitin C
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(use as internal housekeeping gene control of gene UBC for; accurate **normalization** of real-time quant. RT-PCR data by geometric averaging of multiple internal housekeeping gene controls)

REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L95 ANSWER 8 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:101364 CAPLUS
DOCUMENT NUMBER: 134:159830
TITLE: Methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter **DNA** sequencing
INVENTOR(S): Hadd, Andy; Jovanovich, Stevan
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 131 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2001009389	A2	20010208	WO 2000-US21182		20000802
WO 2001009389	A3	20010816			
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG					
US 6423536	B1	20020723	US 2000-577199		20000523
CA 2380794	AA	20010208	CA 2000-2380794		20000802
EP 1203099	A2	20020508	EP 2000-952450		20000802
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL					
JP 2003505110	T2	20030212	JP 2001-513644		20000802
PRIORITY APPLN. INFO.:			US 1999-146732P	P	19990802
			US 2000-577199	A	20000523
			WO 2000-US21182	W	20000802

ED Entered STN: 09 Feb 2001

AB Methods for preparing nanoscale reactions using nucleic acids are presented. Nucleic acids are captured saturably, yet reversibly, on the internal surface of the reaction chamber, typically a capillary. Excess nucleic acid is removed and the reaction is performed directly within the capillary. Alternatively, the saturably bound nucleic acid is eluted, dispensing a metered amount of nucleic acid for subsequent reaction in a sep. chamber. Devices for effecting the methods of the invention and a system designed advantageously to utilize the methods for high throughput

nucleic acid sequencing reactions using capillary array electrophoresis
are also provided.
IC ICM C12Q001-68
CC 9-1 (Biochemical Methods)
Section cross-reference(s): 3, 6
IT Nucleotides, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(2',3'-dideoxyribo-, triphosphates; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Archaebacteria (Archaea)
Bacteriophage
Eukaryote (Eukaryotae)
Plasmid vectors
Plasmids
Prokaryote
Virus
(DNA isolated from; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(DNA, Dye-labeled; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Halides
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(Tetraamine, for immobilizing DNA templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Apparatus
(air-based thermal cycling; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Genetic polymorphism
(amplified fragment length polymorphism; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Capillary electrophoresis
(array; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Biotechnology
(biochips, containing capillary array; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Glass, biological studies
Metals, biological studies
Semimetals
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(channel; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)
IT Denaturants

(chaotropic, for immobilizing DNA templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT DNA formation
(chemical or enzymic; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Thermal cycling
(device for preparing nucleic acid templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Microsatellite DNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(devices for anal. of; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT **Genotyping** (method)
(devices for; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Fluorescent substances
(dideoxynucleotide triphosphates or primer conjugated with; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction)

IT DNA
RL: ANT (Analyte); ANST (Analytical study)
(double-stranded; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT PCR (polymerase chain reaction)
(for preparing nucleic acid templet; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT DNA
RL: ANT (Analyte); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(immobilized; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Capillary tubes
Nanotubes
(methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT DNA
Nucleic acids
RL: ANT (Analyte); ANST (Analytical study)
(methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Deoxyribonucleoside triphosphates
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

IT Oligonucleotides
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(methods and apparatus for nanoscale nucleic acid template capture and

normalization for submicroliter reaction and uses in
submicroliter DNA sequencing for capillary array electrophoresis)
IT RNA
RL: ANT (Analyte); ANST (Analytical study)
(mol. weight distribution of; methods and apparatus for nanoscale nucleic acid
template capture and **normalization** for submicroliter reaction
and uses in submicroliter DNA sequencing for capillary array
electrophoresis)
IT Molecular weight distribution
(of DNA; methods and apparatus for nanoscale nucleic acid template capture
and **normalization** for submicroliter reaction and uses in
submicroliter DNA sequencing for capillary array electrophoresis)
IT DNA
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(primer, Dye-labeled; methods and apparatus for nanoscale nucleic acid
template capture and **normalization** for submicroliter reaction
and uses in submicroliter DNA sequencing for capillary array
electrophoresis)
IT DNA microarray technology
(sequencing from; methods and apparatus for nanoscale nucleic acid template
capture and **normalization** for submicroliter reaction and uses
in submicroliter DNA sequencing for capillary array electrophoresis)
IT DNA
RL: ANT (Analyte); ANST (Analytical study)
(single-stranded; methods and apparatus for nanoscale nucleic acid template
capture and **normalization** for submicroliter reaction and uses
in submicroliter DNA sequencing for capillary array electrophoresis)
IT DNA sequence analysis
(submicroliter; methods and apparatus for nanoscale nucleic acid template
capture and **normalization** for submicroliter reaction and uses
in submicroliter DNA sequencing for capillary array electrophoresis)
IT 64-17-5, Ethanol, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(70%, for washing DNA; methods and apparatus for nanoscale nucleic acid
template capture and **normalization** for submicroliter reaction
and uses in submicroliter DNA sequencing for capillary array
electrophoresis)
IT 50-01-1, Guanidinehydrochloride 56-34-8, Tetraethylammonium chloride
57-13-6, Urea, biological studies 67-68-5, Dimethylsulfoxide, biological
studies 333-20-0, Potassiumthiocyanate 540-72-7, Sodium thiocyanate
593-84-0, Guanidine thiocyanate 650-51-1, Sodium trichloroacetate
7447-41-8, Lithiumchloride, biological studies 7601-89-0, Sodium
perchlorate 7647-15-6, Sodium bromide, biological studies 7681-11-0,
Potassium iodide, biological studies 7681-82-5, Sodium iodide,
biological studies 7758-02-3, Potassium bromide, biological studies
7778-74-7, Potassium perchlorate 16586-14-4, Potassium trichloroacetate
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(for immobilizing DNA templet; methods and apparatus for nanoscale nucleic
acid template capture and **normalization** for submicroliter
reaction and uses in submicroliter DNA sequencing for capillary array
electrophoresis)
IT 9013-05-2, Phosphatase 9014-24-8, RNA polymerase 9031-44-1, Kinase
9031-56-5, Ligase 9032-92-2, Glycosidase 9033-25-4, Methylase
9055-11-2, Endonuclease 9068-38-6, Reverse transcriptase 9075-08-5,
Restriction enzyme 37228-74-3, Exonuclease 80449-01-0, Topoisomerase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(for preparing DNA templets; methods and apparatus for nanoscale nucleic acid
template capture and **normalization** for submicroliter reaction
and uses in submicroliter DNA sequencing for capillary array

electrophoresis)
IT 9012-90-2, DNApolymerase
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(thermostable, for preparing DNA templets; methods and apparatus for nanoscale nucleic acid template capture and **normalization** for submicroliter reaction and uses in submicroliter DNA sequencing for capillary array electrophoresis)

L95 ANSWER 9 OF 31 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:232114 CAPLUS
DOCUMENT NUMBER: 137:211507
TITLE: Evaluation of **normalization** procedures for oligonucleotide array data based on spiked cRNA controls
AUTHOR(S): Hill, Andrew A.; Brown, Eugene L.; Whitley, Maryann Z.; Tucker-Kellogg, Greg; Hunter, Craig P.; Slonim, Donna K.
CORPORATE SOURCE: Department of Genomics, Genetics Institute/Wyeth-ayerst Research, Cambridge, MA, 02140, USA
SOURCE: GenomeBiology [online computer file] (2001), 2(12), No pp. given
CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/2001/2/12/research/0055
PUBLISHER: BioMed Central Ltd.
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English
ED Entered STN: 27 Mar 2002
AB Background: Affymetrix oligonucleotide arrays simultaneously measure the abundances of thousands of mRNAs in biol. samples. Comparability of array results is necessary for the creation of large-scale gene expression databases. The standard strategy for normalizing oligonucleotide array readouts has practical drawbacks. We describe alternative normalization procedures for oligonucleotide arrays based on a common pool of known biotin-labeled cRNAs spiked into each hybridization. Results: We first explore the conditions for validity of the 'constant mean assumption', the key assumption underlying current normalization methods. We introduce 'frequency normalization', a 'spike-in'-based normalization method which ests. array sensitivity, reduces background noise and allows comparison between array designs. This approach does not rely on the constant mean assumption and so can be effective in conditions where standard procedures fail. We also define 'scaled frequency', a hybrid normalization method relying on both spiked transcripts and the constant mean assumption while maintaining all other advantages of frequency normalization. We compare these two procedures to a standard global normalization method using exptl. data. We also use simulated data to estimate accuracy and investigate the effects of noise. We find that scaled frequency is as reproducible and accurate as global normalization while offering several practical advantages. Conclusions: Scaled frequency quantitation is a convenient, reproducible technique that performs as well as global normalization on serial expts. with the same array design, while offering several addnl. features. Specifically, the scaled-frequency method enables the comparison of expression measurements across different array designs, yields ests. of absolute message abundance in cRNA and dets. the sensitivity of individual arrays.
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
ST **normalization** procedures oligonucleotide array data spiked cRNA controls
IT RNA
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(complementary; evaluation of **normalization** procedures for

oligonucleotide array data based on spiked cRNA controls)
IT **Genetic** methods
(frequency **normalization**, a 'spike-in'-based **normalization** which ests. sensitivity, reduces noise and compares array designs; evaluation of **normalization** procedures for oligonucleotide array **data** based on spiked cRNA controls)
IT **Genetic** methods
(scaled frequency, a hybrid **normalization** method relying on spiked transcripts and constant mean assumption; evaluation of **normalization** procedures for oligonucleotide array **data** based on spiked cRNA controls)
IT mRNA
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(scaled-frequency method enables measurements across different array designs, ests. of mRNA abundance and dets. sensitivity; evaluation of **normalization** procedures for oligonucleotide array data based on spiked cRNA controls)
IT **Genetic** methods
(standard global, comparison of frequency **normalizaton** and scaled frequency **normalization** with standard global **normalization**; evaluation of **normalization** procedures for oligonucleotide array **data** based on spiked cRNA controls)
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> => d 195 iall 10-25; d all 195 26;d iall 27-31 195

L95 ANSWER 10 OF 31 JICST-EPlus COPYRIGHT 2005 JST on STN
ACCESSION NUMBER: 1040787618 JICST-EPlus
TITLE: Genetic Method for Floorplan by O-Tree in Consideration of the Initial Solution
AUTHOR: NUMAYAMA KIMIHIKO; ASAI HIDEKI
NINOMIYA HIROSHI
CORPORATE SOURCE: Shizuoka Univ., Fac. Engineering, JPN
Shonan Inst. Technol., Fac. Engineering, JPN
SOURCE: Denshi Joho Tsushin Gakkai Gijutsu Kenkyu Hokoku (IEIC Technical Report (Institute of Electronics, Information and Communication Engineers)), (2004) vol. 104, no. 295(NLP2004 40-53), pp. 7-12. Journal Code: S0532B (Fig. 7, Tbl. 3, Ref. 8)
ISSN: 0913-5685
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Short Communication
LANGUAGE: Japanese
STATUS: New
ABSTRACT:
This report describes the **Genetic** Algorithm for solving the non-slicing structure floorplan problem using Tree representation. Furthermore, we propose the method to generate initial solutions of Tree representation using the **Delaunay Triangulation.** Finally, we demonstrate the validity of the proposed method for MCNC benchmark tests through the computer simulations. (author abst.)

CLASSIFICATION: JE10000A; NC03161C (681.3:658.51; 621.3.049.77)
CONTROLLED TERM: VLSI; layout; floor plan; circuit design; tree structure; genetic algorithm; decomposition method; computer simulation
BROADER TERM: LSI; integrated circuit; micro circuit; micro circuit

technique; technology; design; structure; optimization method; computer application; utilization; simulation

L95 ANSWER 11 OF 31 JICST-EPlus COPYRIGHT 2005 JST on STN
ACCESSION NUMBER: 1000825187 JICST-EPlus
TITLE: Optimum Design Method and Evaluation of Small Sector Antenna Using Cylindrical Coordinate GA-ICT.
AUTHOR: MARUYAMA TAMAMI; HONMA NAOKI; HORI TOSHIKAZU
CORPORATE SOURCE: Nippon Telegraph and Telephone Corp. (NTT), Network Innovation Lab., JPN
SOURCE: Denshi Joho Tsushin Gakkai Gijutsu Kenkyu Hokoku (IEIC Technical Report (Institute of Electronics, Information and Communication Enginners)), (2000) vol. 100, no. 200(SAT2000 29-39), pp. 67-74. Journal Code: S0532B (Fig. 10, Ref. 15)
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
LANGUAGE: Japanese
STATUS: New
ABSTRACT:
We propose a new method for determining the optimum antenna design by combining a **genetic** algorithm(GA) and Improved circuit theory(ICT). Without having to provide initially the basic structure, the GA-ICT method automatically obtains the desired design requirements such as electrical characteristics, antenna shape, and size utilizing an optimization evaluation function. Since the evaluation function is constructed based on the weights derived from the characteristics, it may become difficult to obtain all design requirements at the same time due to the nonlinear characteristics of each item. To overcome this problem, we introduce a vector evaluation method to GA-ICT that generates in parallel calculations different individual sets. The evaluation functions have different weights to generate different chromosomes that satisfy other design conditions in the first parallel GA operation and the sets are merged in the next GA operation. By applying this vector evaluated GA-ICT to the sector antenna down sizing problem, we were able to downsize the multi-sector monopole Yagi-Uda **array** antenna(MSMPYA) by 70%. (author abst.)

CLASSIFICATION: ND06000M (621.396.67)
CONTROLLED TERM: multi-beam antenna; **genetic** algorithm; optimum design; antenna design; Yagi-Uda antenna; cylinder; **coordinate system**; small type
BROADER TERM: beam antenna; antenna(electric); optimization method; design; communication design; end-fire **array** antenna; **array** antenna; linear antenna; hollow body; solid(cubic); type

L95 ANSWER 12 OF 31 JICST-EPlus COPYRIGHT 2005 JST on STN
ACCESSION NUMBER: 960994917 JICST-EPlus
TITLE: Modeling and Integrated Optimum Design of Structure and Control System.
AUTHOR: KAJIWARA ITSURO
CORPORATE SOURCE: Tokyo Inst. of Technol.
SOURCE: Nippon Kikai Gakkai Zenkoku Taikai Koen Ronbunshu, (1996) vol. 74th, no. Vol 5, pp. 82-87. Journal Code: X0587A (Fig. 9, Tbl. 1, Ref. 6)
PUB. COUNTRY: Japan
DOCUMENT TYPE: Conference; Short Communication
LANGUAGE: Japanese
STATUS: New
ABSTRACT:
Approaches for modeling of the system based on modal analysis and integrated optimum design of structure/control system to achieve the high performances concerning the vibration suppression and the high speed positioning are

presented in this paper. In the integrated optimization for the vibration suppression, the structural shape and the sensor/actuator placement are simultaneously optimized based on sensitivity analysis in LQR control system and GA approach in H.INF. control system. In the integrated optimization for the high speed positioning, the desired frequency characteristics of the servosystem are achieved by the integrated optimization of structure and dynamic compensator, and the time history response of the closed-loop system can be improved by the integrated optimization of structure and LQI control system. Application results with simplified models show the effectiveness and the practicability of the proposed approaches. (author abst.)

CLASSIFICATION: IA02030D; HD02000E (681.5.03.015; 624.041/.047)
CONTROLLED TERM: structure analysis; structure(construction); control system; optimum design; concurrency; **coordinate system**; modeling; vibration control; position control; optimum control; sensor **array**; actuator; sensitivity analysis; optimization method; algorithm; structural system; LQG control; **genetic** algorithm
BROADER TERM: analysis; system; design; property; operation(processing); control; sensor; instrumentation element; control equipment; equipment

L95 ANSWER 13 OF 31 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN DUPLICATE 5

ACCESSION NUMBER: 1998-0307624 PASCAL

TITLE (IN ENGLISH): Recognising building patterns using matched filters and genetic search
Extraction of man-made objects from aerial and satellite images
AUTHOR: CROSS A. D. J.; HANCOCK E. R.
LEBERL F. (ed.); KALLIANY R. (ed.); GRUBER M. (ed.)
CORPORATE SOURCE: Department of Computer Science, University of York, York, Y01 5DD, United Kingdom
Austrian Research Centre Seibersdorf, 2444 Seibersdorf, Austria; Institute for Computer Graphics and Vision, Technical University Graz, Muenzgrabenstrasse 11, 8010 Graz, Austria
International Association of Pattern Recognition. Technical Committee 7 (TC-7, "Photogrammetry and Remote Sensing", INT (patr.)
SOURCE: ISPRS journal of photogrammetry and remote sensing, (1998), 53(2), 95-107, 29 refs.
Conference: IAPR TC-7 Workshop "Mapping Buildings, Roads and Other Man-Made Structures from Images", Graz (Austria), 2 Sep 1996
Illustrations
ISSN: 0924-2716
DOCUMENT TYPE: Journal; Conference
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: Netherlands
LANGUAGE: English
AVAILABILITY: INIST-4647, 354000075809890040
ABSTRACT: This paper is concerned with recognising buildings in aerial images. We abstract the images in terms of relational graphs. Specifically, we use **Delaunay triangulations** to represent the arrangement of located buildings. Localisation is realised using matched filters. The filters are trained by drawing upon the duality between convolution in the image domain and multiplication in

the Fourier domain. The matched filters prove to be remarkably stable. We match **Delaunay** graphs representing image pairs using **genetic** search with a Bayesian relational consistency criterion as fitness function. The use of **genetic** search allows us to perform the optimisation without the traditional problems of sensitivity to initial conditions and convergence to local optima.

CLASSIFICATION CODE: 225B04
001E01M04; Universe sciences; Earth sciences; Internal geophysics

CONTROLLED TERM: Austria; urban areas; triangulation; buildings; aerial photography; imagery; stereograms; image analysis

BROADER TERM: Central Europe; Europe

L95 ANSWER 14 OF 31 PASCAL on STN

ACCESSION NUMBER: 2004-0495992 PASCAL

TITLE (IN ENGLISH): A global optimal registration method for satellite remote sensing images
Programmetric computer vision : Graz, 9-13 September 2002

AUTHOR: GONGJIAN WEN; DEREN LI; LIANGPEI ZHANG; XIUXIAO YUAN
KALLIANY R. (ed.); LEBERT F. (ed.)

CORPORATE SOURCE: LIESMARS, Wuhan University, Wuhan, Hubei, China; ATR National Lab National University of Defense Technology, Changsha, Hunan, China
International Society for Photogrammetry and Remote Sensing, United Kingdom (patr.)

SOURCE: The international archives of the photogrammetry, remote sensing and spatial information sciences (Print), (2002), A394-A399, 1 tabl., 8 refs.
Conference: ISPRS Commission III Symposium, Graz (Austria), 9 Sep 2002
Illustrations; Table
ISSN: 1682-1750

DOCUMENT TYPE: Journal; Conference
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United Kingdom
LANGUAGE: English
AVAILABILITY: INIST-Y 34307, 354000124342140630

ABSTRACT: One of the main obstacles in image registration is the precise estimation of a mapping function that determines geometric transformation between two image **coordinate systems.** For conventional image registration methods, their registration results are not the global optimal, and accuracy is low because only a few local **control points** are used for the estimation. In this paper, we develop a global optimal method in order to get a registration approach with high accuracy. In our method, an energy function that is directly related to the parameters of the mapping function is defined in the whole image. Thus, estimation of the global optimal mapping function can be solved through energy optimization. In defining the energy function, we choose a strength measure that is based on contour edge points. It is demonstrated that the strength measure is insensitive to image radiometric

distortion. Therefore, our method is applicable for various kinds of images, even for different sensors images. In order to solve the energy optimization, we design a pipelining hybrid framework that combines **genetic** algorithms (GAs) and a simplex method (SM). The GAs are applied firstly to look for a few initial guesses from some sub-images, and then the SM is employed to get the optima of the energy function near these initial guesses. It is found that the pipelining hybrid framework is not trapped in a local optimum, and converges fast. Hence, one of the advantages of our algorithm is that it successfully avoids advanced feature extraction and feature matching in the image registration. Its characteristics are of automatic and robust. Experimental results have shown that our method can provide better accuracy than the manual registration.

CLASSIFICATION CODE: 225B04
001E01M04; Universe sciences; Earth sciences; Internal geophysics

CONTROLLED TERM: imagery; Space remote sensing; methodology; algorithms; cartography; transformations; **coordinate systems**; accuracy; optimization; distortion

L95 ANSWER 15 OF 31 PASCAL COPYRIGHT 2005 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2001-0063483 PASCAL

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TITLE (IN ENGLISH): Heuristic approach to image registration
Automatic target recognition X : Orlando FL, 26-28 April 2000

AUTHOR: GERTNER Izidor; MASLOV Igor
SADJADI Firooz A. (ed.)

CORPORATE SOURCE: Dept. of Computer Science, City College, City Univ. of New York, United States; Dept. of Computer Science, Graduate School and Univ. Center, City Univ. of New York, United States

SOURCE: SPIE proceedings series, (2000), 4050, 238-244, 3 refs.
Conference: 10 Automatic target recognition. Conference, Orlando FL (United States), 26 Apr 2000
ISSN: 1017-2653
ISBN: 0-8194-3676-3

DOCUMENT TYPE: Journal; Conference
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-21760, 354000092034160270

ABSTRACT: Image registration, i.e. correct mapping of images obtained from different sensor readings onto common reference frame, is a critical part of multi-sensor ATR/AOR systems based on readings from different types of sensors. In order to fuse two different sensor readings of the same object, the readings have to be put into a common **coordinate system**
. This task can be formulated as optimization problem in a space of all possible affine transformations of an image. In this paper, a combination of heuristic methods is explored to register gray-scale images. The modification of **Genetic** Algorithm is used as

the first step in global search for optimal transformation. It covers the entire search space with (randomly or heuristically) scattered probe points and helps significantly reduce the search space to a subspace of potentially most successful transformations. Due to its discrete character, however, **Genetic** Algorithm in general can not converge while coming close to the optimum. Its termination point can be specified either as some predefined number of generations or as achievement of a certain acceptable convergence level. To refine the search, potential optimal subspaces are searched using more delicate and efficient for local search Taboo and Simulated Annealing methods.

CLASSIFICATION CODE: 001B00G07D; Physics; Metrology
001D04A05C; Applied sciences; Information theory, Signal processing

PHYS. AND ASTRONOM.CODE: 0707D

CONTROLLED TERM: Image registration; Multisensor; **Coordinate system**; Measurement sensor; Sensor **array**; Affine transformation; Heuristic approach; Image recognition; Algorithms; Image matching; Total attenuated reflection; Infrared spectroscopy; Theoretical study

L95 ANSWER 16 OF 31 Elsevier BIOBASE COPYRIGHT 2005 Elsevier Science B.V. on STN DUPLICATE

ACCESSION NUMBER: 2004199365 ESBIOBASE

TITLE: Geographic patterns of (genetic, morphologic, linguistic) variation: How barriers can be detected by using Monmonier's algorithm

AUTHOR: Manni F.; Guerard E.; Heyer E.

CORPORATE SOURCE: F. Manni, Dept. Hommes, Natures, Societes, Human Population Genetics Group, CNRS UMR 5145, 17 Place du Trocadero, Paris, France.

SOURCE: Human Biology, (2004), 76/2 (173-190), 35 reference(s)
CODEN: HUBIAA ISSN: 0018-7143

DOCUMENT TYPE: Journal; Article

COUNTRY: United States

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: When sampling locations are known, the association between genetic and geographic distances can be tested by spatial autocorrelation or regression methods. These tests give some clues to the possible shape of the genetic landscape. Nevertheless, correlation analyses fail when attempting to identify where genetic barriers exist, namely, the areas where a given variable shows an abrupt rate of change. To this end, a computational geometry approach is more suitable because it provides the locations and the directions of barriers and because it can show where geographic patterns of two or more variables are similar. In this frame we have implemented Monmonier's (1973) maximum difference algorithm in a new software package to identify genetic barriers. To provide a more realistic representation of the barriers in a genetic landscape, we implemented in the software a significance test by means of bootstrap matrices analysis. As a result, the noise associated with genetic markers can be visualized on a geographic map and the areas where genetic barriers are more robust

can be identified. Moreover, this multiple matrices approach can visualize the patterns of variation associated with different markers in the same overall picture. This improved Monmonier's method is highly reliable and can be applied to nongenetic data whenever sampling locations and a distance matrix between corresponding data are available.

CLASSIFICATION CODE: 99 General

SUPPLEMENTARY TERM: **Genetic** barriers; Monmonier's algorithm; **Delaunay triangulation**; Bootstrap analysis; Gene geogaphy; **Genetic** structures

L95 ANSWER 17 OF 31 INSPEC (C) 2005 IEE on STN DUPLICATE 2

ACCESSION NUMBER: 2003:7697571 INSPEC

DOCUMENT NUMBER: C2003-09-4260-012

TITLE: Mesh optimization for surface approximation using an efficient coarse-to-fine evolutionary algorithm.

AUTHOR: Hui-Ling Huang; Shinn-Ying Ho (Dept. of Inf. Eng., Feng Chia Univ., Taichung, Taiwan)

SOURCE: Pattern Recognition (May 2003) vol.36, no.5, p.1065-81. 24 refs.
Doc. No.: S0031-3203(02)00113-9
Published by: Elsevier
Price: CCCC 0031-3203/03/$30.00
CODEN: PTNRA8 ISSN: 0031-3203
SICI: 0031-3203(200305)36:5L.1065:MOSA;1-8

DOCUMENT TYPE: Journal

TREATMENT CODE: Theoretical

COUNTRY: United Kingdom

LANGUAGE: English

ABSTRACT: The investigated mesh optimization problem C(N, n) for surface approximation, which is NP-hard, is to minimize the global error between a digital surface and its approximating mesh surface by efficiently locating a limited number n of grid points which are a subset of the original N sample points. This paper proposes an efficient coarse-to-fine evolutionary algorithm (CTFEA) with a novel orthogonal **array** crossover (OAX) for solving the mesh optimization problem. OAX adaptively divides the meshes of parents into a number of parts using a tuning parameter for applying a coarse-to-fine technique. Meshes of children are formed from an intelligent combination of the good parts from their parents rather than the conventional random combination. The better one of two parts in two parents is chosen by evaluating the contribution of the individual parts to the fitness function based on orthogonal experimental design. The coarse-to-fine technique of CTFEA can advantageously solve large mesh optimization problems. Furthermore, CTFEA using an additional inheritance technique can further efficiently locate the grid points in the mesh surface. It is shown empirically that CTFEA outperforms the existing evolutionary algorithm in terms of both approximation quality and convergence speed, especially in solving large mesh optimization problems.

CLASSIFICATION CODE: C4260 Computational geometry; C4130 Interpolation and function approximation (numerical analysis); C6130B Graphics techniques

CONTROLLED TERM: EVOLUTIONARY COMPUTATION; **GENETIC**

ALGORITHMS; MESH GENERATION; SURFACE FITTING
SUPPLEMENTARY TERM: mesh optimization; NP-hard; **orthogonal array crossover**; tuning parameter; **Delaunay triangulation**; evolutionary computation; CTFEA; inheritance; **genetic algorithm**; surface approximation

L95 ANSWER 18 OF 31 INSPEC (C) 2005 IEE on STN DUPLICATE 3
ACCESSION NUMBER: 2001:7046174 INSPEC
DOCUMENT NUMBER: C2001-11-4260-018
TITLE: Multicriteria-optimized triangulations.
AUTHOR: Kolingerova, I. (Dept. of Comput. Sci. & Eng., Univ. of West Bohemia, Czech Republic); Ferko, A.
SOURCE: Visual Computer (Aug. 2001) vol.17, no.6, p.380-95. 47 refs.
Published by: Springer-Verlag
CODEN: VICOE5 ISSN: 0178-2789
SICI: 0178-2789(200108)17:6L.380:MOT;1-1
DOCUMENT TYPE: Journal
TREATMENT CODE: Practical; Theoretical
COUNTRY: Germany, Federal Republic of
LANGUAGE: English
ABSTRACT: Triangulation of a given set of points in a plane is one of the most commonly solved problems in computer graphics and computational geometry. Because they are useful in many applications, triangulations must provide well-shaped triangles. Many criteria have been developed to provide such meshes, including weight and angular criteria. Each criterion has its pros and cons, some of them are difficult to compute, and sometimes a polynomial algorithm is not even known. By any of the existing deterministic methods, it is not possible to compute a triangulation which satisfies more than one criterion or which contains parts developed according to several criteria. We explain how such a mixture can be generated using genetic optimization.
CLASSIFICATION CODE: C4260 Computational geometry; C6130B Graphics techniques; C4185 Finite element analysis; C1180 Optimisation techniques
CONTROLLED TERM: COMPUTATIONAL GEOMETRY; COMPUTER GRAPHICS; GENETIC ALGORITHMS; MESH GENERATION
SUPPLEMENTARY TERM: **multicriteria-optimized triangulations**; computer graphics; computational geometry; well-shaped triangles; meshes; weight criteria; angular criteria; polynomial algorithm; deterministic methods; **genetic optimization**; **minimum-weight triangulation**; **Delaunay triangulation**

L95 ANSWER 19 OF 31 INSPEC (C) 2005 IEE on STN DUPLICATE 4
ACCESSION NUMBER: 1998:6050414 INSPEC
DOCUMENT NUMBER: B9811-8380-011; C9811-7410B-093
TITLE: Optimal design of linear oscillatory actuator using genetic algorithm.
AUTHOR: Enomoto, H.; Harada, K.; Ishihara, Y.; Todaka, T. (Dept. of Electr. Eng., Doshisha Univ., Kyoto, Japan); Hirata, K.
SOURCE: IEEE Transactions on Magnetics (Sept. 1998) vol.34, no.5, pt.1, p.3515-18. 5 refs.
Published by: IEEE
Price: CCCC 0018-9464/98/$10.00
CODEN: IEMGAQ ISSN: 0018-9464

SICI: 0018-9464(199809)34:5:1L.3515:ODLO;1-M
Conference: 11th International Conference on Computation of Electromagnetic Fields (COMPUMAG). Rio de Janeiro, Brazil, 3-6 Nov 1997

DOCUMENT TYPE: Conference Article; Journal
TREATMENT CODE: Theoretical
COUNTRY: United States
LANGUAGE: English
ABSTRACT: This paper presents the optimal design method of a linear oscillatory actuator (LOA) using the **genetic** algorithm (GA). In this method, the GA is coupled with a 2D-dynamic analysis code based on the finite element method (FEM) to obtain the optimal geometry which can give a satisfactory dynamic performance. In order to take the motion of the LOA into consideration, the finite element meshes are automatically regenerated using **Delaunay triangulation.** The utility of this method is verified through the comparison of the performances of the optimal geometry and those of the initial geometry.
CLASSIFICATION CODE: B8380 Control gear and apparatus; B8330 Linear machines; B0260 Optimisation techniques; B0290T Finite element analysis; C7410B Power engineering computing; C4185 Finite element analysis; C4260 Computational geometry
CONTROLLED TERM: ELECTRIC ACTUATORS; ELECTRIC MACHINE CAD; GENETIC ALGORITHMS; LINEAR MOTORS; MESH GENERATION
SUPPLEMENTARY TERM: linear oscillatory actuator; design optimisation; **genetic algorithm**; GA; 2D-dynamic analysis code; finite element method; FEM; optimal geometry; dynamic performance; **Delaunay triangulation**; CPU time
ELEMENT TERM: D

L95 ANSWER 20 OF 31 INSPEC (C) 2005 IEE on STN DUPLICATE 7
ACCESSION NUMBER: 1993:4360675 INSPEC
DOCUMENT NUMBER: A9308-9650M-001
TITLE: A spectral analysis of ordinary chondrites, S-type asteroids, and their component minerals: **genetic** implications.
AUTHOR: Fanale, F.P.; Clark, B.E.; Bell, J.F. (Dept. of Geol. & Geophys., Sch. of Ocean & Earth Sci. & Technol., Hawaii Univ., Honolulu, HI, USA)
SOURCE: Journal of Geophysical Research (25 Dec. 1992) vol.97, no.E12, p.20863-74. 75 refs.
Price: CCCC 0148-0227/92/92JE-02228$05.00
CODEN: JGREA2 ISSN: 0148-0227
DOCUMENT TYPE: Journal
TREATMENT CODE: Bibliography; Experimental
COUNTRY: United States
LANGUAGE: English
ABSTRACT: Three salient features of visible and infrared reflectance spectra of ordinary chondrites (OCs) and S-type asteroids are albedo at 0.56 mu m; continuum slope; and depth of the electronic absorption band due to octahedrally coordinated Fe2+ in olivine and pyroxene. These quantities were numerically extracted from the spectra of 23 OCs and 39 S-type asteroids to be plotted in a three-dimensional **coordinate system.** When the region containing the 39 S-asteroid spectra is compared with that of the

altered and unaltered OCs, it is found that not one of the OCs falls within the S-asteroid region. The range of S-asteroid parameters is then compared with potential pure 'end-member' components most likely to result from magmatic differentiation of a chondritic protoasteroid: olivine, orthopyroxene, clinopyroxene, and Fe,Ni meteorite metal. The S-asteroid **array** is consistent with random mixtures of the differentiated components. The S-asteroids may supply achondrites, irons, and stony irons to Earth rather than well-mixed breccias of these components.

CLASSIFICATION CODE: A9650M Meteorites, micrometeorites; A9630H Asteroids; A9635E Chemical composition; A9580J Photographic region; A9580G Infrared

CONTROLLED TERM: ALBEDO; ASTEROIDS; ASTRONOMICAL SPECTRA; INFRARED ASTRONOMICAL OBSERVATIONS; METEORITES; MINERALS; VISIBLE ASTRONOMICAL OBSERVATIONS

SUPPLEMENTARY TERM: stony meteorites; asteroid-meteorite connection; differentiated mineral components mixture; near-IR; metallic component spectrum; 560-nm albedo; near-UV; absorption band depth; stony-Fe meteorites; small chondritic asteroids metamorphism; EM induction heating; asteroids heating; spectral analysis; ordinary chondrites; S-type asteroids; component minerals; visible; infrared reflectance spectra; continuum slope; electronic absorption band; olivine; pyroxene; **three-dimensional coordinate system** ; magmatic differentiation; chondritic protoasteroid; orthopyroxene; clinopyroxene; achondrites; stony irons; 300 to 2500 nm; 560 nm; octahedrally coordinated Fe2+; Fe-Ni meteorite metal; FeMgSiO4; FeMgSiO3; Fe meteorites; 26Al decay heating

CHEMICAL INDEXING: FeNi bin, Fe bin, Ni bin; FeMgSiO4 ss, SiO4 ss, Fe ss, Mg ss, O4 ss, Si ss, O ss; FeMgSiO3 ss, Fe ss, Mg ss, O3 ss, Si ss, O ss; Fe el; Al el; Fe el

PHYSICAL PROPERTIES: wavelength 3.0E-07 to 2.5E-06 m; wavelength 5.6E-07 m

ELEMENT TERM: S; Cs*O; OCs; O cp; cp; Cs cp; Fe; Fe2+; Fe ip 2; ip 2; 23OCs; is; O is; 23O; 39S; S is; Ni; Fe*Ni; Fe sy 2; sy 2; Ni sy 2; Fe-Ni; Fe*Mg*O*Si; Fe sy 4; sy 4; Mg sy 4; O sy 4; Si sy 4; FeMgSiO4; Fe cp; Mg cp; Si cp; FeMgSiO3; Al; 26Al; Al is; FeNi; Ni cp; FeMgSiO; O*Si; SiO; Mg; O; Si

L95 ANSWER 21 OF 31 INSPEC (C) 2005 IEE on STN

ACCESSION NUMBER: 2004:8248174 INSPEC

DOCUMENT NUMBER: C2005-03-1180-002

TITLE: An improved genetic algorithm to solve the Euclidean plane TSP by using geometry structure.

AUTHOR: Pan Liang; Zhu Hua-yong; Shen Lin-cheng; Chang Wen-sen (Coll. of Mechatronics Eng. & Autom., National Univ. of Defense Technol., Changsha, China)

SOURCE: Journal of National University of Defense Technology (Oct. 2004) vol.26, no.5, p.109-14. 21 refs.
Published by: Editorial Department J. Natl. Univ. Def. Technol
CODEN: GKDXEM ISSN: 1001-2486
SICI: 1001-2486(200410)26:5L.109:IGAS;1-E

DOCUMENT TYPE: Journal

TREATMENT CODE: Theoretical; Experimental

COUNTRY: China

LANGUAGE: Chinese

ABSTRACT: The TSP is a classic combinatorial optimization

problem. According to the character of the optimal tour of Euclidean plane TSP problem, the sub-path and related notions are presented. A tour construction algorithm is designed by using convex hull, and a **genetic** algorithm is improved to solve the problem by using **Delaunay triangulation** diagram as heuristic information. The experimental results in the 144 cities in China and other TSP instances show that the algorithm is effective.

CLASSIFICATION CODE: C1180 Optimisation techniques; C4260 Computational geometry; C4185 Finite element analysis
CONTROLLED TERM: GENETIC ALGORITHMS; MESH GENERATION
SUPPLEMENTARY TERM: **improved genetic algorithm**; Euclidean plane TSP; geometry structure; combinatorial optimization problem; tour construction algorithm; convex hull; **Delaunay triangulation diagram**; heuristic information; China; traveling salesman problem

L95 ANSWER 22 OF 31 INSPEC (C) 2005 IEE on STN
ACCESSION NUMBER: 2003:7790823 INSPEC
DOCUMENT NUMBER: B2004-01-6135-042; C2004-01-5260B-038
TITLE: Extraction of outlines in arbitrary shape from binary images using genetic algorithm.
AUTHOR: Abe, M.; Ouchi, T.; Kawamata, M. (Graduate Sch. of Eng., Tohoku Univ., Sendai, Japan)
SOURCE: Transactions of the Institute of Electronics, Information and Communication Engineers D-II (July 2003) vol.J86D-II, no.7, p.1036-48. 12 refs.
Published by: Inst. Electron. Inf. & Commun. Eng
CODEN: DTGDE7 ISSN: 0915-1923
SICI: 0915-1923(200307)J86DII:7L.1036:EOAS;1-4
DOCUMENT TYPE: Journal
TREATMENT CODE: Practical; Theoretical
COUNTRY: Japan
LANGUAGE: Japanese
ABSTRACT: This paper proposes a method to extract outlines in arbitrary shapes from images using **genetic** algorithm (GA). The target images are binary images including disconnected outlines and noise. The proposed method can extract outlines recognized by human visual ability. In this method, **Delaunay triangulation** is first used to obtain a graph including the outline. Second, vertices and edges locally recognized as noise in the graph are eliminated. Finally, from the graph for which noise has been reduced, the outlines is extracted using GA, where the polygons in the graph are coded into chromosomes. Experimental results show that the proposed method can extract an outline of arbitrary shape from the image. Moreover, the proposed method is extended to extract multiple outlines. Experimental results also show the extended method can extract all outlines in the image.
CLASSIFICATION CODE: B6135 Optical, image and video signal processing; B0260 Optimisation techniques; C5260B Computer vision and image processing techniques; C1180 Optimisation techniques; C1250M Image recognition; C4260 Computational geometry
CONTROLLED TERM: EDGE DETECTION; FEATURE EXTRACTION; GENETIC ALGORITHMS; IMAGE DENOISING; MESH GENERATION
SUPPLEMENTARY TERM: arbitrary shape; binary image; **genetic**

algorithm; disconnected outline; human visual ability; **Delaunay triangulation**; noise elimination; outline extraction

L95 ANSWER 23 OF 31 INSPEC (C) 2005 IEE on STN
ACCESSION NUMBER: 2003:7547323 INSPEC
DOCUMENT NUMBER: B2003-04-6135E-042; C2003-04-1250M-048
TITLE: Extraction of outlines in arbitrary shape using genetic algorithm.
AUTHOR: Ouchi, T.; Abe, M.; Kawamata; M.
SOURCE: Record of Electrical and Communication Engineering Conversazione Tohoku University (Oct. 2002) vol.71, no.1, p.421-2. 6 refs.
Published by: Tohoku Univ
CODEN: TDDDAI ISSN: 0385-7719
SICI: 0385-7719(200210)71:1L.421:EOAS;1-3
DOCUMENT TYPE: Journal
TREATMENT CODE: Theoretical; Experimental
COUNTRY: Japan
LANGUAGE: Japanese
ABSTRACT: This paper proposes a method to extract outlines in arbitrary shape from images using a **Genetic** Algorithm (GA). The target images are binary images including disconnected outlines and noise. The proposed method can extract outlines recognized by human visual ability. In this method, **Delaunay triangulation** is first used to obtain a graph including the outline. Second, vertexes and edges locally recognized as noise in the graph are eliminated. Finally, from the graph of which the noise has been reduced, the outline is extracted using GA, where the polygons in the graph are coded into chromosomes. Experimental results show that the proposed method can extract an outline of arbitrary shape from the image. Moreover, the proposed method is extended to extract multiple outlines. Experimental results also show that the extended method can extract all outlines in the image.
CLASSIFICATION CODE: B6135E Image recognition; B0260 Optimisation techniques; C1250M Image recognition; C1180 Optimisation techniques; C5260B Computer vision and image processing techniques
CONTROLLED TERM: FEATURE EXTRACTION; GENETIC ALGORITHMS; GRAPH THEORY; IMAGE RECOGNITION
SUPPLEMENTARY TERM: arbitrary shape outlines; outline extraction; multiple outlines; image processing; **genetic algorithm** ; binary images; disconnected outlines; noise; **Delaunay triangulation**; graph; polygon coding; chromosomes

L95 ANSWER 24 OF 31 INSPEC (C) 2005 IEE on STN
ACCESSION NUMBER: 1997:5573108 INSPEC
DOCUMENT NUMBER: C9706-4260-065
TITLE: A genetic algorithm for the minimum weight triangulation.
AUTHOR: Kaihuai Qin; Wenping Wang (Dept. of Comput. Sci., Hong Kong Univ., Hong Kong); Minglun Gong
SOURCE: Proceedings of 1997 IEEE International Conference on Evolutionary Computation (ICEC '97) (Cat. No.97TH8283) New York, NY, USA: IEEE, 1997. p.541-6 of xv+724 pp. 17 refs.
Conference: Indianapolis, IN, USA, 13-16 April 1997

Sponsor(s): IEEE; IEEE Neural Netowrk Council (NNC); Evolutionary Computation (ICEC '97)
Price: CCCC 0 7803 3949 5/97/$10.00
ISBN: 0-7803-3949-5

DOCUMENT TYPE: Conference Article
TREATMENT CODE: Theoretical
COUNTRY: United States
LANGUAGE: English
ABSTRACT: In this paper, a new method for the minimum weight triangulation of points on a plane, called genetic minimum weight triangulation (GMWT), is presented based on the rationale of genetic algorithms. Polygon crossover and its algorithm for triangulations are proposed. New adaptive genetic operators, or adaptive crossover and mutation operators, are introduced. It is shown that the new method for the minimum weight triangulation can obtain more optimal results of triangulations than the greedy algorithm.
CLASSIFICATION CODE: C4260 Computational geometry; C1180 Optimisation techniques; C4185 Finite element analysis
CONTROLLED TERM: COMPUTATIONAL GEOMETRY; GENETIC ALGORITHMS; MESH GENERATION
SUPPLEMENTARY TERM: **genetic algorithm**; GMWT; **genetic minimum weight triangulation**; polygon crossover; **adaptive genetic operators**; adaptive crossover; mutation operators; greedy algorithm; **Delaunay triangulation**

L95 ANSWER 25 OF 31 INSPEC (C) 2005 IEE on STN
ACCESSION NUMBER: 1994:4834992 INSPEC
DOCUMENT NUMBER: B9501-6140C-218; C9501-5260B-121
TITLE: A **genetic** algorithm approach to camera calibration in 3D machine vision.
AUTHOR: Roberts, M.; Naftel, A.J. (Dept. of Math. & Stat., Central Lancashire Univ., Preston, UK)
SOURCE: IEE Colloquium on 'Genetic Algorithms in Image Processing and Vision' (Digest No.1994/193)
London, UK: IEE, 1994. p.12/1-5 of 78 pp. 13 refs.
Conference: London, UK, 20 Oct 1994
Sponsor(s): IEE
DOCUMENT TYPE: Conference Article
TREATMENT CODE: Theoretical
COUNTRY: United Kingdom
LANGUAGE: English
ABSTRACT: The camera calibration problem in 3D machine vision involves the determination of the interior orientation (internal camera geometry) and exterior orientation parameters (position and angular rotation relative to a specified 3D world **coordinate system**) using known **control points**. Additional parameters can be used to model the nonlinear effects of lens distortion. If an unknown targeted point is then imaged in two cameras or single camera together with an active structured light source (e.g. a projector), the position of the object point can be determined by intersecting the two calibrated rays.
CLASSIFICATION CODE: B6140C Optical information, image and video signal processing; B7130 Measurement standards and calibration; B0260 Optimisation techniques; C5260B Computer vision and image processing techniques; C1180 Optimisation techniques

CONTROLLED TERM: CALIBRATION; COMPUTER VISION; **GENETIC** ALGORITHMS; STEREO IMAGE PROCESSING
SUPPLEMENTARY TERM: 3D machine vision; camera calibration; **genetic algorithm**; interior orientation; internal camera geometry; exterior orientation; position; angular rotation; lens distortion nonlinear effects; active structured light source
ELEMENT TERM: D

L95 ANSWER 26 OF 31 COMPUSCIENCE COPYRIGHT 2005 FIZ KARLSRUHE on STN
DUPLICATE 6
AN 1998(3):MA59507 COMPUSCIENCE
TI Optimal tetrahedral mesh generation for three-dimensional point set.
AU Qin, Kaihuai; Wu, Bian; Guan, Youjiang; Ge, Zhenzhou
SO Sci. China, Ser. E. (1997) v. 40(2) p. 135-143.
1997.
DT Journal
TC Theoretical
CY Germany, Federal Republic of
LA English
IP FIZKA
DN 881.68126
AB Three-dimensional (3D) **triangulation** is a basic topic in computer graphics. It is considered very difficult to obtain the global optimal 3D **triangulation**, such as the **triangulation** which satisfies the max-min solid angle criterion. A new method called **genetic** tetrahedral mesh generation algorithm (GTMGA for short) is presented. GTMGA is based on the principle of **genetic** algorithm and aims at the global optimal **triangulation.** With a multiobjective fitness function, GTMGA is able to perform optimizations for different requirements. New crossover operator and mutation operator, polyhedron crossover and polyhedron mutation, are used in GTMGA. It is shown by the experimental results that GTMGA works better than both the 3D **Delaunay triangulation** and the algorithm based on local transformations. (Summary)
CC *I.3.5 Computational geometry and object modeling
ST computer graphics; Delaunay triangulation.

L95 ANSWER 27 OF 31 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-635295 [61] WPIDS
DOC. NO. NON-CPI: N2004-502124
TITLE: Helical conebeam computed tomography imaging system performs exact reconstruction of conebeam data projected from native scan coordinates of x-ray detector **array**, into image representation.
DERWENT CLASS: S03 S05 T01
INVENTOR(S): BROWN, K M; HEUSCHER, D J; NOO, F N; PACK, J D
PATENT ASSIGNEE(S): (PHIG) KONINK PHILIPS ELECTRONICS NV
COUNTRY COUNT: 108
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2004072905	A1	20040826	(200461)*	EN	36	G06T011-00

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE
LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE
DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ
OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG
US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004072905	A1	WO 2004-IB386	20040209

PRIORITY APPLN. INFO: US 2003-482380P 20030625; US 2003-447426P 20030214
INT. PATENT CLASSIF.:
MAIN: G06T011-00
BASIC ABSTRACT:
WO2004072905 A UPAB: 20040923
NOVELTY - An X-ray source (12) arranged transversely to a helical trajectory, produces X-ray conebeam and directs it to the examination region. A X-ray detector **array** (14) detects conebeam from the examination region, and generates projection data in its nature scan coordinates. Several processors perform an exact reconstruction of the conebeam projection data from native scan coordinates, into an image representation.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for reconstruction method for reconstructing conebeam computed tomography.

USE - Helical conebeam computed tomography imaging system.

ADVANTAGE - Fast and exact image reconstruction of conebeam imaging data is performed, by simplified image reconstruction computations by **transforming** tomographic **projection** data to detector independent voxel based **coordinate system.**

DESCRIPTION OF DRAWING(S) - The figure shows a helical conebeam computed tomography imaging system including exact reconstruction of acquired conebeam projection data.

X-ray source 12
examination region 14
X-detector **array** 16
back projector 42,82
derivative processor 60
convolution processor 64
Dwg.1/6
FILE SEGMENT: EPI
FIELD AVAILABILITY: AB; GI
MANUAL CODES: EPI: S03-E06B3; S05-D02A1; S05-D02A5E; T01-J06A; T01-J10C4B

L95 ANSWER 28 OF 31 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-532852 [50] WPIDS
DOC. NO. CPI: C2003-144068
TITLE: Identifying similar surface motifs of **molecular** sequences by identifying surface motifs and subsequences, generating comparison metrics, calculating statistical significance and identifying **molecular** sequences.
DERWENT CLASS: B04 J04
INVENTOR(S): ADAMIAN, L; BINKOWSKI, T A; LIANG, J; BINKOWSKI, A T
PATENT ASSIGNEE(S): (ADAM-I) ADAMIAN L; (BINK-I) BINKOWSKI T A; (LIAN-I) LIANG J; (UNII) UNIV ILLINOIS FOUND
COUNTRY COUNT: 100
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 2003048724	A2	20030612	(200350)*	EN	85	G01N000-00

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
US 2003149537	A1	20030807	(200358)			G06F019-00
AU 2002365755	A1	20030617	(200419)			G01N000-00

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003048724	A2	WO 2002-US38030	20021127
US 2003149537	A1 Provisional	US 2001-333969P	20011129
	Provisional	US 2001-334689P	20011130
		US 2002-306296	20021127
AU 2002365755	A1	AU 2002-365755	20021127

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002365755	A1 Based on	WO 2003048724

PRIORITY APPLN. INFO: US 2001-334689P 20011130; US 2001-333969P 20011129; US 2002-306296 20021127

INT. PATENT CLASSIF.:
MAIN: G01N000-00; G06F019-00

BASIC ABSTRACT:

WO2003048724 A UPAB: 20030805

NOVELTY - Identifying similar surface motifs of molecular sequences comprises identifying surface motifs of molecular sequences and sub-sequences having groups of atoms from the molecular sequences associated with surface motifs, generating comparison metrics, calculating statistical significance of at least one comparison metric and identifying molecular sequences similar to the molecular sequences.

USE - Used for identifying similar surface motifs of molecular sequences.

ADVANTAGE - The method takes into account the nature of the surface features and geometric orientation.

DESCRIPTION OF DRAWING(S) - The drawing shows an alternative flow diagram for identifying similar molecular structures.

Dwg.9/9

FILE SEGMENT: CPI
FIELD AVAILABILITY: AB; GI; DCN
MANUAL CODES: CPI: B04-C02; B04-C03; B04-E01; B04-E03; B04-N04; B11-C08; B11-C08F; B12-K04E; J04-C02

L95 ANSWER 29 OF 31 WPIDS

ACCESSION NUMBER: 2001-201924 [20] WPIDS
DOC. NO. NON-CPI: N2001-143968
DOC. NO. CPI: C2001-059902
TITLE: Classification of **molecules**, for e.g. assisting with the selection of chemical compounds for further study, by forming a three-dimensional body representative

of structure of the **molecule**, and generating structural descriptors.

DERWENT CLASS: B04 J04 S03
INVENTOR(S): EDELSBRUNNER, H; LIANG, J
PATENT ASSIGNEE(S): (EDEL-I) EDELSBRUNNER H; (LIAN-I) LIANG J
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
US 6182016	B1	20010130	(200120)*		19	G01N033-50

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 6182016	B1	US 1997-918624	19970822

PRIORITY APPLN. INFO: US 1997-918624 19970822
INT. PATENT CLASSIF.:
MAIN: G01N033-50
BASIC ABSTRACT:

US 6182016 B UPAB: 20010410

NOVELTY - Molecules are classified by forming a three-dimensional body representative of structure of the molecule; generating structural descriptors reflecting structural information about neighboring atomic centers or groups of atomic centers of the molecule; and classifying the molecule using the descriptors by identifying values associated with the descriptors.

DETAILED DESCRIPTION - Classification of molecules comprises (i) forming a 3-dimensional body representative of structure of the molecule by placing a potentially overlapping ball around each atom or group of atoms of the molecule; (ii) generating structural descriptors reflecting structural information about neighboring atomic centers or groups of atomic centers of the molecule; and (iii) classifying the molecule using the descriptors by identifying values associated with the descriptors. The ball has a radius for the particular type of atom or group of atoms. The structural descriptors relate to a Voronoi diagram corresponding to the 3-dimensional body.

INDEPENDENT CLAIMS are also included for:

(a) an electronic storage device comprising a storage medium which stores a computer program for implementing the specified classification method;

(b) a method of identifying molecules that are similar to a known compound by classifying the known compound based on the above method, identifying significant elements in the classification method in terms of classification parameters, determining classifications of relevant molecules having the identified classification parameters similar or identical with the known compounds, and establishing the structure of a molecule corresponding to the determined classification of relevant molecules;

(c) a method of evaluating the degree of similarity between two molecules by determining the degree of similarity between the two compounds based on a comparison of the descriptors determined for each molecule; and

(d) a method of selecting and evaluating the efficacy of a chemical compound using a chemical or pharmacological test.

USE - The method is used for assisting with the selection of chemical compounds for further study; for identifying and evaluating similarities and differences between molecules that may be reflected in the behavior of the molecules; and for computing 3-dimensional descriptors useful in

3-dimensional sub-structure searching, similarity searching, combinatorial chemistry, library design, and diversity management. Molecular descriptors are of central importance for developing high throughput screening for drug lead searching and drug lead optimization.

ADVANTAGE - The method provides an accurate and efficient approach for computing 3-dimensional descriptors.

Dwg.0/8

FILE SEGMENT: CPI EPI
FIELD AVAILABILITY: AB
MANUAL CODES: CPI: B11-C08; B12-K04E; J04-B01
EPI: S03-E14H

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ACCESSION NUMBER: 2000-039199 [03] WPIDS
DOC. NO. NON-CPI: N2000-029533
TITLE: Three dimensional object surface feature reconstruction generating system for determining actual 3D shapes and volumes of objects.
DERWENT CLASS: T01
INVENTOR(S): ALBECK, D; SHASHUA, A
PATENT ASSIGNEE(S): (COGN-N) COGNITENS LTD; (YISS) YISSUM RES & DEV CO
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
WO 9959100	A1	19991118	(200003)*	EN	29	G06K009-00
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE						
W: CA JP						
EP 1194881	A1	20020410	(200232)	EN		G06K009-00
R: DE FR GB						

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9959100	A1	WO 1999-IB1226	19990514
EP 1194881	A1	EP 1999-950370	19990514
		WO 1999-IB1226	19990514

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1194881	A1 Based on	WO 9959100

PRIORITY APPLN. INFO: US 1998-96359P 19980813; US 1998-85501P 19980514
INT. PATENT CLASSIF.:
MAIN: G06K009-00
BASIC ABSTRACT:

WO 9959100 A UPAB: 20000118

NOVELTY - A post-**transformation projective** representation generator is configured to generate post-**transformation projective** representation in relation to relationships between epipoles in respective image planes for images in each of pre- transformation image set and post-transformation image set.

DETAILED DESCRIPTION - The pre-transformation image set comprise images recorded prior to transformation. The post- transformation image set comprise images recorded subsequent to transformation. An Euclidian representation generator produce Euclidian representation of surface element in scene, using post- **transformation projection**

and **projective**-to-Euclidian matrix. INDEPENDENT CLAIMS are also included for the following:

(a) 3D object surface feature reconstruction generating method;

(b) 3D object surface feature reconstruction generating program

USE - For determining actual 3D shapes and volumes of objects, and also for computer vision and robotics.

ADVANTAGE - Facilitates reconstruction using images recorded by cameras. **Control points** are available in scene as recorded following non-rigid transformation.

DESCRIPTION OF DRAWING(S) - The figure shows flowchart of Euclidian reconstruction generator.

Dwg.3/4

FILE SEGMENT: EPI
FIELD AVAILABILITY: AB; GI
MANUAL CODES: EPI: T01-J10C4; T01-S02

L95 ANSWER 31 OF 31 WPIDS
ACCESSION NUMBER: 1983-B7985K [06] WPIDS
DOC. NO. NON-CPI: N1983-023277
TITLE: Correcting for aberrations in photogrammetric projection - using four reference marks with automatic metering on projected plane of aerial photograph.
DERWENT CLASS: P82 P83 S02 S06
INVENTOR(S): SPATA, P
PATENT ASSIGNEE(S): (JENA) JENOPTIK JENA GMBH; (KOCH-I) KOCH R
COUNTRY COUNT: 4
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG	MAIN IPC
DE 3214050	A	19830203	(198306)*		7	
DD 200820	A	19830615	(198341)			
US 4482223	A	19841113	(198448)			
CH 656223	A	19860613	(198630)			
DD 200820	B	19870121	(198720)			

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 4482223	A	US 1982-388687	19820615

PRIORITY APPLN. INFO: DD 1981-231974 19810722
INT. PATENT CLASSIF.: G01C011-04; G03B023-08; G03B027-68; G03C005-00
BASIC ABSTRACT:

DE 3214050 A UPAB: 19930925

The original aerial photograph (B) is exposed to four reference markings (1,2,3,4) in the four quadrants, before processing. When projected onto a plan (P) the automatic focus control for the lens (O) monitors the fit of the reference markings and provides a best possible fit.

The projector is linked to a processor which ensures that any lens aberration is catered for with the larger magnifications. The system operates automatically and rapidly and compensates for inclination, curvature etc. which would otherwise lead to false perspective.

1/1

FILE SEGMENT: EPI GMPI
FIELD AVAILABILITY: AB
MANUAL CODES: EPI: S02-B04; S06-B04A

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